

Method BLASTX
NCBI GI g3914442
BLAST score 419
E value 2.0e-41
Match length 105
% identity 79

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi 1916350 (U92504) PSI-H subunit [Brassica rapa]

. No. 163396

Seq. No. 163396 Seq. ID LIB3177-062-P1-K1-E11

Method BLASTX
NCBI GI g3136033
BLAST score 183
E value 2.0e-13
Match length 87

% identity 44
NCBI Description (AL023590) putative metallopeptidase [Schizosaccharomyces

pombe]

Seq. No. 163397

Seq. ID LIB3177-062-P1-K1-E12

Method BLASTX
NCBI GI g3915823
BLAST score 300
E value 1.0e-27
Match length 57
% identity 100

NCBI Description [Segment 1 of 2] 60S RIBOSOMAL PROTEIN L5

Seq. No. 163398

Seq. ID LIB3177-062-P1-K1-E2

Method BLASTX
NCBI GI g2493144
BLAST score 191
E value 1.0e-14
Match length 58
% identity 71

NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE

16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__\$60132

H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis

thaliana]

Seq. No. 163399

Seq. ID LIB3177-062-P1-K1-E3

Method BLASTX
NCBI GI g4512685
BLAST score 469
E value 9.0e-64
Match length 155
% identity 79

NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]

>gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

NCBI Description



163400

```
Seq. No.
Seq. ID
                  LIB3177-062-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  q2264311
BLAST score
                  210
E value
                  1.0e-114
Match length
                  251
                   96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163401
Seq. ID
                  LIB3177-062-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q544425
BLAST score
                   429
E value
                  2.0e-42
Match length
                  83
                  100
% identity
                  GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN)
NCBI Description
                  >gi 419756 pir S30148 glycine-rich protein (clone AtGRP8)
                   - Arabidopsis thaliana >gi 16305 emb CAA78712 (Z14988)
                   glycine rich protein [Arabidopsis thaliana] >gi 166658
                   (L04171) ORF [Arabidopsis thaliana] >gi 166839 (L00649)
                   RNA-binding protein [Arabidopsis thaliana]
Seq. No.
                  163402
Seq. ID
                  LIB3177-062-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g4741952
BLAST score
                  278
E value
                  1.0e-24
Match length
                   60
                   90
% identity
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  163403
                  LIB3177-062-P1-K1-E7
Seq. ID
Method
                  BLASTX
                  g1477480
NCBI GI
BLAST score
                  704
E value
                  1.0e-74
Match length
                  145
                   99
% identity
                  (U40341) carbamoyl phosphate synthetase large chain
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  163404
                  LIB3177-062-P1-K1-E8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1871577
BLAST score
                  188
                  2.0e-14
E value
Match length
                  52
                   65
% identity
```

(Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. ID



```
163405
Seq. No.
                  LIB3177-062-P1-K1-F1
Seq. ID
Method
                  BLASTX
                  q2252828
NCBI GI
BLAST score
                  455
E value
                  2.0e-45
Match length
                  121
                  80
% identity
                  (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  163406
                  LIB3177-062-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128217
BLAST score
                   473
                  2.0e-47
E value
Match length
                  110
                   87
% identity
                   (AC004077) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3337374 (AC004481) hypothetical protein [Arabidopsis
                   thaliana]
                   163407
Seq. No.
                  LIB3177-062-P1-K1-F11
Seq. ID
                   BLASTX
Method
                   g1773014
NCBI GI
BLAST score
                   300
                   2.0e-27
E value
                   89
Match length
                   70
% identity
                  (Y10338) chloride channel Stclc1 [Solanum tuberosum]
NCBI Description
Seq. No.
                   163408
                   LIB3177-062-P1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2062161
BLAST score
                   678
                   2.0e-71
E value
                   140
Match length
                   50
% identity
                   (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                   thaliana]
                   163409
Seq. No.
                   LIB3177-062-P1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3885511
BLAST score
                   366
                   4.0e-35
E value
                   95
Match length
                   79
% identity
NCBI Description
                   (AF084200) similar to PSI-K subunit of photosystem I from
                   barley [Medicago sativa]
                   163410
```

21800

LIB3177-062-P1-K1-F4



```
Method
                   BLASTX
NCBI GI
                   g4741960
                   574
BLAST score
E value
                   2.0e-59
Match length
                   128
% identity
                   85
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
                   163411
Seq. No.
Seq. ID
                   LIB3177-062-P1-K1-F5
Method
                   BLASTN
NCBI GI
                   g4249393
BLAST score
                   103
E value
                   6.0e-51
Match length
                   131
% identity
                   95
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T9J23 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163412
Seq. ID
                   LIB3177-062-P1-K1-F6
Method
                   BLASTX
NCBI GI
                   g2104957
BLAST score
                   584
E value
                   2.0e-60
Match length
                   107
% identity
                   100
NCBI Description (U96924) immunophilin [Arabidopsis thaliana]
                   163413
Seq. No.
Seq. ID
                   LIB3177-062-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   g3413714
BLAST score
                   364
E value
                   7.0e-35
Match length
                   105
% identity
                   22
                  (AC004747) putative myrosinase-binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   163414
Seq. ID
                   LIB3177-062-P1-K1-F8
Method
                   BLASTN
NCBI GI
                   g3985958
BLAST score
                   286
E value
                   1.0e-160
Match length
                   419
% identity
                   99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MZN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163415
Seq. ID
                  LIB3177-062-P1-K1-F9
Method
                  BLASTN
```

NCBI GI g2760167 BLAST score 127 E value 3.0e-65

```
Match length
                   246
% identity
                   100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MCO15, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163416
Seq. ID
                   LIB3177-062-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g2088662
BLAST score
                   605
E value
                   6.0e-63
Match length
                   140
% identity
                   85
NCBI Description
                  (AF002109) unknown protein [Arabidopsis thaliana]
Seq. No.
                   163417
                   LIB3177-062-P1-K1-G10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4220632
BLAST score
                   164
E value
                   4.0e-87
Match length
                   429
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K6M13, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163418
Seq. ID
                   LIB3177-062-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   g2500378
BLAST score
                   464
E value
                   2.0e-46
Match length
                   95
% identity
                   92
NCBI Description 60S RIBOSOMAL PROTEIN L37
Seq. No.
                  163419
Seq. ID
                  LIB3177-062-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q3286693
BLAST score
                  450
E value
                  4.0e-58
Match length
                  125
% identity
NCBI Description
                  (Y15433) 33 kDa polypeptide of oxygen-evolving complex
                   (OEC) in photosystem II [Arabidopsis thaliana]
```

Seq. ID LIB3177-062-P1-K1-G3

Method BLASTN
NCBI GI 94090568
BLAST score 114
E value 1.0e-57
Match length 186
% identity 97

NCBI Description Arabidopsis thaliana Myb-related transcription factor CCA1

gene, complete cds



```
Seq. No.
                   163421
Seq. ID
                   LIB3177-062-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g2500497
BLAST score
                   314
E value
                   7.0e-29
Match length
                   72
% identity
                   78
NCBI Description
                  40S RIBOSOMAL PROTEIN S21 >gi 1419372 emb CAA67225.1
                   (X98656) ribosomal protein S21 [Zea mays]
Seq. No.
                   163422
Seq. ID
                   LIB3177-062-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g115385
BLAST score
                   62
E value
                   6.0e-67
Match length
                  132
                   99
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  163423
Seq. ID
                  LIB3177-062-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g1732570
BLAST score
                  713
E value
                  1.0e-75
Match length
                  157
% identity
                  85
NCBI Description (U72153) beta-glucosidase [Arabidopsis thaliana]
                  163424
Seq. No.
Seq. ID
                  LIB3177-062-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g2062161
BLAST score
                  735
E value
                  3.0e-78
Match length
                  139
% identity
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  163425
Seq. ID
                  LIB3177-062-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q3286693
BLAST score
                  611
E value
                  9.0e-64
Match length
                  125
% identity
NCBI Description
                  (Y15433) 33 kDa polypeptide of oxygen-evolving complex
```

(OEC) in photosystem II [Arabidopsis thaliana]



```
Seq. ID
                   LIB3177-062-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g3096931
BLAST score
                   576
E value
                   1.0e-59
Match length
                   113
% identity
                   99
NCBI Description
                  (AL023094) putative ribosomal protein S16 [Arabidopsis
                  thaliana]
Seq. No.
                  163427
Seq. ID
                  LIB3177-062-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  g2281081
BLAST score
                  227
E value
                  1.0e-125
Match length
                  227
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC F18019 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163428
                  LIB3177-062-P1-K1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2351062
BLAST score
                  210
E value
                  1.0e-114
Match length
                  362
% identity
                  98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAH20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163429
Seq. ID
                  LIB3177-062-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g2199574
BLAST score
                  340
E value
                  2.0e-32
Match length
                  65
% identity
                  98
NCBI Description (AF004293) aquaporin [Brassica rapa]
Seq. No.
                  163430
Seq. ID
                  LIB3177-062-P1-K1-H3
Method
                  BLASTX
                  g3914658
                  294
```

NCBI GI BLAST score E value 5.0e-27 Match length 74 % identity 80

50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR NCBI Description

>gi_1694974_emb_CAA70851_ (Y09635) plastid ribosomal

protein [Arabidopsis thaliana]

Seq. No. 163431

Seq. ID LIB3177-062-P1-K1-H4

Method BLASTX



NCBI GI g2506443 BLAST score 553 E value 6.0e-57 Match length 139 % identity 78

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,

CHLOROPLAST >gi_2117520_pir__JQ1285

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde

3-phosphate dehydrogenase [Arabidopsis thaliana]

>gi_1402885_emb_CAA66816_ (X98130)

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) [Arabidopsis thaliana]

Seq. No. 163432

Seq. ID LIB3177-062-P1-K1-H5

Method BLASTX
NCBI GI g113026
BLAST score 372
E value 9.0e-63
Match length 135
% identity 87

NCBI Description ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)

>gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape

>gi_255220_bbs_112862 isocitrate lyase, threo-D

S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf 1913424A

isocitrate lyase [Brassica napus]

Seq. No. 163433

Seq. ID LIB3177-062-P1-K1-H6

Method BLASTX
NCBI GI g4741952
BLAST score 98

E value 8.0e-66 Match length 125 % identity 60

NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No. 163434

Seq. ID LIB3177-062-P1-K1-H7

Method BLASTX
NCBI GI g132090
BLAST score 618
E value 2.0e-64
Match length 113
% identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR

(RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir RKMUB1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B1 precursor - Arabidopsis thaliana >gi 16193 emb CAA32700 (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 163435



Seq. ID LIB3177-062-P1-K1-H9

Method BLASTN
NCBI GI 94587641
BLAST score 165
E value 1.0e-87
Match length 286
% identity 99

NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic

sequence, complete sequence

Seq. No. 163436

Seq. ID LIB3177-063-P1-K1-A12

Method BLASTN
NCBI GI g3047100
BLAST score 90
E value 2.0e-43
Match length 122
% identity 94

NCBI Description Arabidopsis thaliana BAC F6N23

Seq. No. 163437

Seq. ID LIB3177-063-P1-K1-A3

Method BLASTN
NCBI GI g4756963
BLAST score 280
E value 1.0e-156
Match length 326
% identity 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23

(ESSA project)

Seq. No. 163438

Seq. ID LIB3177-063-P1-K1-A4

Method BLASTX
NCBI GI g2661422
BLAST score 442
E value 3.0e-57
Match length 122
% identity 94

NCBI Description (AJ001342) Putative S-phase-specific ribosomal protein

[Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_(AL023094) Putative S-phase-specific ribosomal protein

[Arabidopsis thaliana]

Seq. No. 163439

Seq. ID LIB3177-063-P1-K1-A5

Method BLASTX
NCBI GI g3157947
BLAST score 361
E value 7.0e-35
Match length 74
% identity 53

NCBI Description (AC002131) Similar to protein gb_Z74962 from Brassica

oleracea which is similar to bacterial YRN1 and HEAHIO proteins. ESTs gb_T21954, gb_T04283, gb_Z37609, gb_N37366, gb_R90704, gb_F15500 and gb_F14353 come from this gene.

[Arabidopsis tha



```
Seq. No.
                   163440
Seq. ID
                   LIB3177-063-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   g3892722
BLAST score
                   534
E value
                   1.0e-54
Match length
                   120
% identity
                   92
NCBI Description (AL033545) putative protein [Arabidopsis thaliana]
Seq. No.
                  163441
                  LIB3177-063-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                   a121075
BLAST score
                   259
                   5.0e-23
E value
Match length
                   63
% identity
                   84
NCBI Description
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi 166725
                   (M82921) H-Protein precursor [Arabidopsis thaliana]
                  >gi_861215 (U27144) glycine decarboxylase complex H-protein
                  precursor [Arabidopsis thaliana] >gi_3608151 (AC005314)
                  glycine decarboxylase complex H-protein [Arabidopsis
                  thaliana] >gi_445119 prf__1908425A Gly
                  decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]
Seq. No.
                  163442
Seq. ID
                  LIB3177-063-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q115385
BLAST score
                  216
E value
                  5.0e-18
Match length
                  43
% identity
                  100
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  163443
Seq. ID
                  LIB3177-063-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  g4455262
BLAST score
                  97
E value
                  2.0e-47
Match length
                  217
% identity
                  58
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
                  (ESSAII project)
```

Seq. ID LIB3177-063-P1-K1-B12

Method BLASTX
NCBI GI g4587564
BLAST score 364
E value 1.0e-72
Match length 145

```
100 Miles (100 Miles (
```

```
% identity
                   (AC006550) Strong similarity to gb_X14017 photosystem I
NCBI Description
                   reaction centre subunit II precursor (psaD) from Spinacia
                   oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb T14133,
                   gb_N65521, gb_T424\overline{9}8, gb_T419\overline{1}8, gb_N380\overline{2}4
Seq. No.
                   163445
Seq. ID
                   LIB3177-063-P1-K1-B2
Method
                   BLASTN
NCBI GI
                   g4757417
BLAST score
                   236
E value
                   1.0e-130
Match length
                   364
% identity
                   99
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   T30G6, complete sequence
Seq. No.
                   163446
Seq. ID
                   LIB3177-063-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   g1170247
BLAST score
                   324
E value
                   1.0e-30
Match length
                   64
% identity
                   89
NCBI Description HEVEIN-LIKE PROTEIN PRECURSOR >gi 407248 (U01880)
                   pre-hevein-like protein [Arabidopsis thaliana]
Seq. No.
                   163447
Seq. ID
                   LIB3177-063-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g418405
BLAST score
                   45
E value
                   1.0e-09
Match length
                   82
% identity
                   45
NCBI Description
                   HYPOTHETICAL 55.9 KD PROTEIN IN GDA1-UTR2 INTERGENIC REGION
                   >gi_320711_pir__S30838 hypothetical protein YEL041w - yeast
                   (Saccharomyces cerevisiae) >gi_603638 (U18779) Yel041wp
                   [Saccharomyces cerevisiae]
Seq. No.
                   163448
Seq. ID
                   LIB3177-063-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   g4056502
BLAST score
                   115
E value
                   1.0e-36
Match length
                  102
% identity
                   84
NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
```

Seq. ID LIB3177-063-P1-K1-B6 Method BLASTX

Method BLASTX
NCBI GI g3236246
BLAST score 450
E value 4.0e-45



Match length 89
% identity 93
NCBI Description (AC004684) putative expansin protein [Arabidopsis thaliana]
Seq. No. 163450
Seq. ID LIB3177-063-P1-K1-B7
Method BLASTX

Method BLASTX
NCBI GI g132110
BLAST score 343
E value 1.0e-32
Match length 69
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702 (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 163451

Seq. ID LIB3177-063-P1-K1-B9

Method BLASTX
NCBI GI g2688824
BLAST score 200
E value 4.0e-16
Match length 53
% identity 72

NCBI Description (U93273) putative auxin-repressed protein [Prunus

armeniaca]

Seq. No. 163452

Seq. ID LIB3177-063-P1-K1-C10

Method BLASTN
NCBI GI g16470
BLAST score 107
E value 2.0e-53
Match length 159
% identity 92

NCBI Description Arabidopsis thaliana mRNA for rubisco activase

Seq. No. 163453

Seq. ID LIB3177-063-P1-K1-C12

Method BLASTX
NCBI GI g4455248
BLAST score 461
E value 3.0e-46
Match length 105
% identity 96

NCBI Description (AL035523) acyl carrier-like protein [Arabidopsis thaliana]

Seq. No. 163454

Seq. ID LIB3177-063-P1-K1-C2

Method BLASTN
NCBI GI g4757409
BLAST score 71
E value 1.0e-31
Match length 389



```
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MVC8, complete sequence
Seq. No.
                   163455
                  LIB3177-063-P1-K1-C5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4733953
BLAST score
                  138
E value
                   1.0e-71
Match length
                   285
% identity
                   94
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F13011 genomic
                   sequence, complete sequence
Seq. No.
                  163456
Seq. ID
                  LIB3177-063-P1-K1-C6
Method
                  BLASTX
                  g1488604
NCBI GI
BLAST score
                  147
E value
                  2.0e-09
Match length
                  36
% identity
                  86
NCBI Description (Z49842) ribulosebiphosphate carboxylase [Hordeum lechleri]
Seq. No.
                  163457
Seq. ID
                  LIB3177-063-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  q4757405
BLAST score
                  154
E value
                  3.0e-81
Match length
                  347
                  97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MOJ10, complete sequence
Seq. No.
                  163458
Seq. ID
                  LIB3177-063-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  g3046849
BLAST score
                  209
E value
                  1.0e-114
Match length
                  213
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K18L3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163459
Seq. ID
                  LIB3177-063-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g1170939
BLAST score
                  687
E value
                  1.0e-72
Match length
                  139
```

% identity 93
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)

```
>gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon
```

esculentum]

NCBI Description Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 163461

Seq. ID LIB3177-063-P1-K1-D11

Method BLASTX
NCBI GI g3738340
BLAST score 360
E value 1.0e-34
Match length 80
% identity 81

NCBI Description (AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No. 163462

Seq. ID LIB3177-063-P1-K1-D12

Method BLASTX
NCBI GI g399013
BLAST score 261
E value 4.0e-23
Match length 54
% identity 94

NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)

>gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis

thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549)

adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator

[Arabidopsis thaliana]

Seq. No. 163463

Seq. ID LIB3177-063-P1-K1-D3

Method BLASTN
NCBI GI 94539415
BLAST score 142
E value 3.0e-74
Match length 210
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA

project)

Seq. No. 163464

Seq. ID LIB3177-063-P1-K1-D4

Method BLASTN NCBI GI g4584387



```
BLAST score
                   53
E value
                   3.0e-21
Match length
                   124
% identity
                   94
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7
NCBI Description
                   (ESSA project)
Seq. No.
                   163465
Seq. ID
                   LIB3177-063-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   g3834310
BLAST score
                   644
E value
                   1.0e-67
Match length
                   130
% identity
                   98
NCBI Description
                   (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
                   gb D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464,
                   gb_N37265, gb_H36151, gb_Z34711, gb AA040983, and gb T22122
                   come from this gene. [Arabidopsis thaliana]
Seq. No.
                   163466
Seq. ID
                   LIB3177-063-P1-K1-D7
Method
                   BLASTN
NCBI GI
                   g2262135
BLAST score
                   202
E value
                  1.0e-110
Match length
                   241
% identity
                   96
NCBI Description
                  Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
                  cM, complete sequence
Seq. No.
                   163467
Seq. ID
                  LIB3177-063-P1-K1-D8
Method
                  BLASTN
NCBI GI
                  q4741959
BLAST score
                  34
E value
                  5.0e-10
Match length
                  41
% identity
                  98
NCBI Description
                  Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete
Seq. No.
                  163468
Seq. ID
                  LIB3177-063-P1-K1-D9
Method
                  BLASTX
                  g135467
                  208
                  4.0e-17
```

NCBI GI BLAST score E value Match length 39 % identity

NCBI Description TUBULIN BETA-4 CHAIN >gi_2129546_pir__S68122 beta-tubulin 4

- Arabidopsis thaliana >gi 166640 (M21415) beta-tubulin

[Arabidopsis thaliana]

Seq. No. 163469

Seq. ID LIB3177-063-P1-K1-E10

Method BLASTX

```
NCBI GI
                   g3123745
BLAST score
                   230
E value
                   2.0e-19
Match length
                   83
% identity
                   52
NCBI Description (AB013447) aluminum-induced [Brassica napus]
Seq. No.
                   163470
Seq. ID
                   LIB3177-063-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g132110
BLAST score
                   161
E value
                   1.0e-11
                   34
Match length
% identity
                   97
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                   B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   163471
Seq. ID
                  LIB3177-063-P1-K1-E12
Method
                  BLASTX
NCBI GI
                   q4586256
BLAST score
                   447
E value
                   2.0e-44
Match length
                   129
% identity
                   72
NCBI Description
                  (AL049640) probable photosystem I chain XI precursor
                   [Arabidopsis thaliana]
Seq. No.
                   163472
Seq. ID
                  LIB3177-063-P1-K1-E2
Method
                  BLASTN
NCBI GI
                   q3169309
BLAST score
                  51
E value
                   7.0e-20
Match length
                   67
% identity
                   94
NCBI Description Arabidopsis thaliana nucleoside diphosphate kinase type 1
                   (NDPK1) gene, complete cds
Seq. No.
                  163473
```

Seq. ID LIB3177-063-P1-K1-E3

Method BLASTX NCBI GI g1175013 BLAST score 331 E value 2.0e-31 78 Match length % identity 87

NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542 pir S44084

plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic

protein 2a [Arabidopsis thaliana]

% identity

99



```
Seq. No.
                   163474
Seq. ID
                   LIB3177-063-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g1916290
BLAST score
                   215
                   2.0e-17
E value
Match length
                   72
                   51
% identity
NCBI Description (U89876) ALY [Mus musculus]
Seq. No.
                  163475
Seq. ID
                  LIB3177-063-P1-K1-E7
                  BLASTN
Method
NCBI GI
                  g3702734
BLAST score
                   302
E value
                   1.0e-169
Match length
                   334
% identity
                   97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNB8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163476
Seq. ID
                  LIB3177-063-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q1345592
BLAST score
                  381
E value
                  5.0e-37
Match length
                  83
% identity
                  95
NCBI Description 14-3-3-LIKE PROTEIN GF14 EPSILON >gi 1022778 (U36446) GF14
                  epsilon isoform [Arabidopsis thaliana]
Seq. No.
                  163477
Seq. ID
                  LIB3177-063-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g2119846
BLAST score
                  601
E value
                  3.0e-68
Match length
                  144
% identity
                  94
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi_16364_emb CAA45790 (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  163478
Seq. ID
                  LIB3177-063-P1-K1-F11
Method
                  BLASTN
NCBI GI
                  g3510247
BLAST score
                  209
E value
                  1.0e-114
Match length
                  408
```

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NCBI Description Arabidopsis thaliana chromosome II BAC F19D11 genomic



sequence, complete sequence [Arabidopsis thaliana] Seq. No. 163479 Seq. ID LIB3177-063-P1-K1-F12 Method BLASTX g548355 NCBI GI BLAST score 459 E value 4.0e-46 Match length 100 % identity 91 NCBI Description NITRATE REDUCTASE 1 (NR1) >gi_486751_pir__\$35228 nitrate reductase (NADH) (EC 1.6.6.1) 1 - Arabidopsis thaliana \geq gi_22757_emb_CAA79494_ (Z19050) nitrate reductase [Arabidopsis thaliana] >gi_448286_prf__1916406A nitrate reductase [Arabidopsis thaliana] Seq. No. 163480 Seq. ID LIB3177-063-P1-K1-F2 Method BLASTX NCBI GI g136636 BLAST score 288 E value 9.0e-26 Match length 75 % identity 80 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir_ S43781 ubiquitin-conjugating enzyme UBC1 -Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi 2981894 pdb 2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana] Seq. No. 163481 Seq. ID LIB3177-063-P1-K1-F3 Method BLASTX NCBI GI q1363489 BLAST score 691 E value 4.0e-73 Match length 128 % identity 99 thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis NCBI Description thaliana >gi_984052_emb_CAA61592 (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana] Seq. No. 163482 Seq. ID LIB3177-063-P1-K1-F4 Method BLASTX NCBI GI q4678260 BLAST score 497 E value 3.0e-50

Match length 121 86

NCBI Description (AL049657) putative protein [Arabidopsis thaliana]

Seq. No. 163483



Seq. ID LIB3177-063-P1-K1-F5 Method BLASTN NCBI GI g3510247 BLAST score 35 E value 3.0e-10 Match length 47 % identity 94 NCBI Description Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 163484 Seq. ID LIB3177-063-P1-K1-F6 Method BLASTX NCBI GI q4586111 BLAST score 227 E value 1.0e-18 Match length 78 % identity 65 NCBI Description (AL049638) putative protein [Arabidopsis thaliana] Seq. No. 163485 Seq. ID LIB3177-063-P1-K1-F7 Method BLASTN NCBI GI g4581084 BLAST score 121 E value 1.0e-61 Match length 280 % identity NCBI Description Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence Seq. No. 163486 Seq. ID LIB3177-063-P1-K1-F8 Method BLASTN NCBI GI g4582437 BLAST score 86 E value 6.0e-41 Match length 171 % identity 99 NCBI Description Arabidopsis thaliana chromosome II BAC F7024 genomic sequence, complete sequence Seq. No. 163487 Seq. ID LIB3177-063-P1-K1-F9 BLASTX g4585935 735 3.0e-78

Method NCBI GI BLAST score E value Match length 140 99 % identity

NCBI Description (AC007211) putative chlorophyll A/B binding protein

[Arabidopsis thaliana] >gi_4741946 gb AAD28770.1 AF134123 1

(AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No. 163488

LIB3177-063-P1-K1-G10 Seq. ID

Method BLASTX



```
NCBI GI
                   q4454048
BLAST score
                   61
E value
                   4.0e-70
Match length
                   131
% identity
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                  163489
Seq. ID
                  LIB3177-063-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                   531
E value
                  7.0e-65
Match length
                  129
% identity
                  98
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  163490
Seq. ID
                  LIB3177-063-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q1076308
BLAST score
                  428
E value
                  3.0e-42
Match length
                  123
% identity
                  72
                  RNA-binding protein cp33 precursor - Arabidopsis thaliana
NCBI Description
                  >gi_681910_dbj_BAA06522_ (D31714) cp33 [Arabidopsis
                  thaliana]
Seq. No.
                  163491
Seq. ID
                  LIB3177-063-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q4204266
BLAST score
                  323
E value
                  1.0e-53
Match length
                  128
% identity
                  93
NCBI Description (AC005223) 52263 [Arabidopsis thaliana]
Seq. No.
                  163492
Seq. ID
                  LIB3177-063-P1-K1-G8
                  BLASTX
                  g132074
                  602
                  9.0e-63
                  110
```

Method NCBI GI BLAST score E value Match length % identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain Al precursor - Arabidopsis thaliana

```
Seq. No.
                   163493
Seq. ID
                   LIB3177-063-P1-K1-G9
Method
                   BLASTN
NCBI GI
                   g1843627
BLAST score
                   70
E value
                   4.0e-31
Match length
                   126
% identity
                   89
NCBI Description
                  Arabidopsis thaliana SNF5 homolog BSH (bsh) mRNA, complete
Seq. No.
                   163494
Seq. ID
                  LIB3177-063-P1-K1-H1
Method
                  BLASTX
NCBI GI
                   g2506496
BLAST score
                   663
E value
                   9.0e-70
Match length
                   128
% identity
                   99
NCBI Description
                  GLUTATHIONE S-TRANSFERASE ERD11 (CLASS PHI)
                  >gi_1890156_emb_CAA72413_ (Y11727) gluthatione
                  S-transferase [Arabidopsis thaliana]
Seq. No.
                  163495
Seq. ID
                  LIB3177-063-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  q4584351
BLAST score
                  346
E value
                  0.0e+00
Match length
                  390
% identity
                  97
NCBI Description Arabidopsis thaliana chromosome II BAC T12H3 genomic
                  sequence, complete sequence
Seq. No.
                  163496
Seq. ID
                  LIB3177-063-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  g2244991
BLAST score
                  152
E value
                  5.0e-80
Match length
                  282
% identity
                  98
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
```

Seq. ID LIB3177-063-P1-K1-H2

fragment No

Method BLASTX
NCBI GI g4539316
BLAST score 535
E value 8.0e-55
Match length 121
% identity 93

NCBI Description (AL035679) putative fructose-bisphosphate aldolase

[Arabidopsis thaliana]

NCBI Description



```
Seq. No.
                    163498
                    LIB3177-063-P1-K1-H3
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4337175
BLAST score
                    591
E value
                    2.0e-61
Match length
                    133
% identity
                    89
NCBI Description
                   (AC006416) ESTs gb T20589, gb T04648, gb AA597906,
                    gb_{T04111}, gb_{R84180}, gb_{R654\overline{2}8}, gb_{T444\overline{3}9}, gb_{T76570},
                    gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                    gb AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   163499
Seq. ID
                   LIB3177-063-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g1732570
BLAST score
                   774
E value
                   8.0e-83
Match length
                   145
% identity
                   98
NCBI Description (U72153) beta-glucosidase [Arabidopsis thaliana]
Seq. No.
                   163500
Seq. ID
                   LIB3177-063-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g2129562
BLAST score
                   707
E value
                   6.0e-75
Match length
                   139
% identity
                   96
NCBI Description
                   class III ADH, glutathione-dependent formaldehyde
                   dehydrogenase. - Arabidopsis thaliana
                   >gi_1143388_emb_CAA57973_ (X82647) class III ADH,
                   glutathione-dependent formaldehyde dehydrogenase.
                   [Arabidopsis thaliana]
Seq. No.
                   163501
Seq. ID
                   LIB3177-063-P1-K1-H6
Method
                   BLASTN
NCBI GI
                   g4584351
BLAST score
                   410
E value
                   0.0e + 00
Match length
                   446
% identity
                   98
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T12H3 genomic
                   sequence, complete sequence
Seq. No.
                   163502
Seq. ID
                   LIB3177-063-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g4204274
BLAST score
                   783
E value
                   8.0e-84
Match length
                   142
% identity
```

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(AC004146) ribulose bisphosphate carboxylase, small subunit

163508



[Arabidopsis thaliana]

Seq. No. 163503 Seq. ID LIB3177-064-P1-K1-A1 Method BLASTX NCBI GI g1769905 BLAST score 365 E value 7.0e-35 Match length 112 % identity 64 NCBI Description (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana] Seq. No. 163504 Seq. ID LIB3177-064-P1-K1-A11 Method BLASTX NCBI GI g2213884 BLAST score 439 E value 1.0e-43 Match length 119 % identity 73 NCBI Description (AF004166) 2-isopropylmalate synthase [Lycopersicon pennellii] Seq. No. 163505 Seq. ID LIB3177-064-P1-K1-A2 Method BLASTN NCBI GI g2264306 BLAST score 457 E value 0.0e + 00Match length 457 % identity 100 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana] Seq. No. 163506 LIB3177-064-P1-K1-A3 Seq. ID Method BLASTN g3540210 NCBI GI BLAST score 54 E value 2.0e-22 Match length 54 % identity 100 NCBI Description Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 163507 Seq. ID LIB3177-064-P1-K1-A4 Method BLASTX NCBI GI g3193285 BLAST score 497 E value 2.0e-50 Match length 99 % identity NCBI Description (AF069298) T14P8.18 gene product [Arabidopsis thaliana]

```
Address to
```

```
Seq. ID
                   LIB3177-064-P1-K1-A5
Method
                   BLASTX
                   g1764100
NCBI GI
BLAST score
                   348
E value
                   7.0e - 33
Match length
                   67
% identity
                   99
NCBI Description
                  (U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis
                   thaliana]
                   163509
Seq. No.
                  LIB3177-064-P1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3142289
BLAST score
                   455
E value
                   2.0e-45
Match length
                   94
% identity
                   90
NCBI Description
                  (AC002411) Strong similarity to beta-keto-Coa synthase
                   gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
Seq. No.
                  163510
Seq. ID
                  LIB3177-064-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g2492952
BLAST score
                  224
E value
                  1.0e-18
Match length
                  95
% identity
                  88
NCBI Description CHORISMATE SYNTHASE 1 PRECURSOR
                   (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1)
                  >gi_542026_pir__S40410 chorismate synthase (EC 4.6.1.4) 1
                  precursor - tomato >gi_410482_emb_CAA79859_ (Z21796)
                  chorismate synthase 1 [Lycopersicon esculentum]
Seq. No.
                  163511
Seq. ID
                  LIB3177-064-P1-K1-A9
Method .
                  BLASTN
NCBI GI
                  q2264307
BLAST score
                  344
E value
                  0.0e+00
Match length
                  445
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MED24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163512
Seq. ID
                  LIB3177-064-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g1710530
BLAST score
                  758
E value
                  6.0e-81
Match length
                  141
                  99
% identity
NCBI Description
                 60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256
```

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ribosomal protein L27a - Arabidopsis thaliana

>gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein

NCBI GI

E value Match length

BLAST score

g4538963

330 9.0e-31

68



L27a [Arabidopsis thaliana]

```
Seq. No.
                   163513
Seq. ID
                   LIB3177-064-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2499535
BLAST score
                   145
E value
                   3.0e-09
Match length
                   32
% identity
                   78
NCBI Description 2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi_595681
                   (U13238) 2-oxoglutarate/malate translocator [Spinacia
                  oleracea]
Seq. No.
                  163514
Seq. ID
                  LIB3177-064-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g3785991
BLAST score
                   368
E value
                   2.0e-35
Match length
                  79
% identity
                  92
NCBI Description (AC005560) putative MAP kinase [Arabidopsis thaliana]
Seq. No.
                  163515
                  LIB3177-064-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131381
BLAST score
                  355
E value
                  3.0e - 34
Match length
                  69
% identity
                  97
NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi_99745_pir__$11852
                  photosystem II oxygen-evolving complex protein 1 precursor
                   - Arabidopsis thaliana >gi_22571_emb_CAA36675_ (X52428) 33
                  kDa oxygen-evolving protein [Arabidopsis thaliana]
Seq. No.
                  163516
Seq. ID
                  LIB3177-064-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  g2245031
BLAST score
                  408
E value
                  0.0e+00
Match length
                  431
% identity
                  99
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  163517
Seq. ID
                  LIB3177-064-P1-K1-B4
Method
                  BLASTX
```



```
% identity
NCBI Description
                  (AL049488) chlorophyll a/b-binding protein-like
                   [Arabidopsis thaliana] >gi_4741958 gb AAD28776.1 AF134129 1
                   (AF134129) Lhcb5 protein [Arabidopsis thaliana]
Seq. No.
                  163518
Seq. ID
                  LIB3177-064-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g4538963
BLAST score
                  366
E value
                  2.0e-58
Match length
                  143
% identity
                  76
NCBI Description
                  (AL049488) chlorophyll a/b-binding protein-like
```

[Arabidopsis thaliana] >gi_4741958 gb AAD28776.1 AF134129 1 (AF134129) Lhcb5 protein [Arabidopsis thaliana] Seq. No. 163519

Seq. ID LIB3177-064-P1-K1-B6 Method BLASTN NCBI GI g4757405 BLAST score 133 E value 1.0e-68 Match length 426

% identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MOJ10, complete sequence

Seq. No. 163520 Seq. ID LIB3177-064-P1-K1-B7 Method BLASTX NCBI GI g1168200 BLAST score 324 4.0e-30

99

E value Match length 80 % identity 88

NCBI Description 14-3-3-LIKE PROTEIN GF14 PSI (14-3-3-LIKE PROTEIN RCI1)

>gi_1361988_pir__S57277 GF14 protein psi chain -

Arabidopsis thaliana >gi_166717 (L09110) GF14 psi chain [Arabidopsis thaliana] >gi_487789 (U09375) GF14psi isoform

[Arabidopsis thaliana]

Seq. No. 163521

Seq. ID LIB3177-064-P1-K1-B9

Method BLASTX NCBI GI q3367536 BLAST score 415 E value 2.0e-46 Match length 99 % identity

(AC004392) Contains similarity to symbiosis-related like NCBI Description

protein F1N20.80 gi_2961343 from A. thaliana BAC gb AL022140. EST gb_T04695 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 163522

Seq. ID LIB3177-064-P1-K1-C10



Method BLASTX NCBI GI a541858 BLAST score 614 E value 8.0e-64 Match length 127 % identity

NCBI Description endoxyloglucan transferase - Arabidopsis thaliana

>gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
transferase [Arabidopsis thaliana] >gi_4063757 (AC005561)

endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No. 163523

LIB3177-064-P1-K1-C3 Seq. ID

Method BLASTX NCBI GI q136636 BLAST score 469 E value 5.0e-47 Match length 87 % identity 99

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -Arabidopsis thaliana >gi_442594 pdb_1AAK Ubiquitin Conjugating Enzyme (E.C. $\overline{6}$.3.2.1 $\overline{9}$) > $\overline{g}i_29\overline{8}1894$ _pdb_2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi 431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 163524

Seq. ID LIB3177-064-P1-K1-C5

Method BLASTX NCBI GI g2956690 BLAST score 433 E value 6.0e-43Match length 116 % identity 58

(AJ223306) PSBY [Arabidopsis thaliana] >gi 3414928 NCBI Description (AF079800) PsbY precursor [Arabidopsis thaliana]

Seq. No. 163525

Seq. ID LIB3177-064-P1-K1-C6

Method BLASTX NCBI GI q2506443 BLAST score 279 E value 4.0e-25 Match length 87 % identity 69

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR.

CHLOROPLAST >gi_2117520_pir__JQ1285
glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde

3-phosphate dehydrogenase [Arabidopsis thaliana]

>gi_1402885_emb_CAA66816_ (X98130)

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) [Arabidopsis thaliana]

```
Seq. No.
                   163526
                   LIB3177-064-P1-K1-C7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g313151
BLAST score
                   42
E value
                   4.0e-14
Match length
                   74
                   95
% identity
NCBI Description A.thaliana ribosomal protein S15 mRNA, complete CDS
Seq. No.
                   163527
                   LIB3177-064-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4467099
BLAST score
                   388
                   8.0e-38
E value
                  80
Match length
                   95
% identity
NCBI Description
                  (AL035538) glycine hydroxymethyltransferase like protein
                   [Arabidopsis thaliana]
Seq. No.
                   163528
Seq. ID
                  LIB3177-064-P1-K1-C9
Method
                  BLASTX
NCBI GI
                   q4263718
BLAST score
                   786
E value
                   4.0e-84
Match length
                   157
% identity
                   98
NCBI Description
                  (AC006223) putative DNA topoisomerase III beta [Arabidopsis
                   thaliana]
Seq. No.
                  163529
                  LIB3177-064-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3688182
BLAST score
                   604
E value
                  8.0e-63
Match length
                  125
% identity
                   90
NCBI Description (AL031804) P-Protein - like protein [Arabidopsis thaliana]
Seq. No.
                  163530
                  LIB3177-064-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132102
BLAST score
                  463
E value
                  1.0e-46
Match length
                  87
                  95
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                  B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_
```

21825

thaliana]

(X14564) ribulose bisphosphate carboxylase [Arabidopsis

```
Seq. No.
                   163531
Seq. ID
                   LIB3177-064-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   g2252828
BLAST score
                   489
E value
                   2.0e-49
Match length
                   118
% identity
                   85
NCBI Description
                  (AF013293) No definition line found [Arabidopsis thaliana]
Seq. No.
                   163532
Seq. ID
                   LIB3177-064-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g4586047
BLAST score
                   519
E value
                   7.0e-53
Match length
                   138
                   75
% identity
NCBI Description
                   (AC007020) putative ferritin protein [Arabidopsis thaliana]
                   >gi 4588004 gb AAD25945.1 AF085279 18 (AF085279)
                   hypothetical ferritin subunit [Arabidopsis thaliana]
Seq. No.
                   163533
Seq. ID
                   LIB3177-064-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   q1514977
BLAST score
                   305
E value
                   5.0e-28
Match length
                   84
% identity
                   79
NCBI Description (D84669) VM23 [Raphanus sativus]
Seq. No.
                   163534
Seq. ID
                   LIB3177-064-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g3894186
BLAST score
                   555
E value
                   3.0e-57
Match length
                   118
% identity
                   91
NCBI Description
                   (AC005662) putative embryo-abundant protein [Arabidopsis
                   thaliana]
Seq. No.
                   163535
Seq. ID
                   LIB3177-064-P1-K1-D5
Method
                  BLASTN
NCBI GI
                   q3643588
BLAST score
                   104
E value
                   2.0e-51
Match length
                   292
```

% identity NCBI Description 1

MCBI Description Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 163536

Seq. ID LIB3177-064-P1-K1-D6



```
Method
                   BLASTX
                   g2499609
NCBI GI
BLAST score
                   280
E value
                   3.0e-25
Match length
                   53
% identity
                   100
NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 5 (MAP KINASE 5)
                   (ATMPK5) >gi_629546_pir__S40471 mitogen-activated protein
                   kinase 5 (EC 2.7.1.-) - Arabidopsis thaliana
                   >gi_457402_dbj_BAA04868_ (D21841) MAP kinase [Arabidopsis
                   thaliana]
Seq. No.
                   163537
Seq. ID
                  LIB3177-064-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g4218120
BLAST score
                  461
E value
                  4.0e-46
Match length
                  116
% identity
                  78
NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  163538
Seq. ID
                  LIB3177-064-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g3212869
BLAST score
                  809
E value
                  7.0e-87
Match length
                  153
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  163539
Seq. ID
                  LIB3177-064-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  q4584351
BLAST score
                  284
E value
                  1.0e-159
Match length
                  336
% identity
                  96
NCBI Description Arabidopsis thaliana chromosome II BAC T12H3 genomic
                  sequence, complete sequence
Seq. No.
                  163540
Seq. ID
                  LIB3177-064-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g132166
BLAST score
                  161
E value
                  3.0e-11
Match length
                  56
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                  PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048
                  ribulose-bisphosphate carboxylase activase precursor -
```

21827

Arabidopsis thaliana >gi_16471_emb_CAA32429 (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]



Seq. ID LIB3177-064-P1-K1-E11

Method BLASTX NCBI GI g132074 BLAST score 472 E value 1.0e-47Match length 96 % identity 95

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 163542

Seq. ID LIB3177-064-P1-K1-E2

Method BLASTX NCBI GI g131398 58 BLAST score E value 3.0e-49Match length 137 % identity 78

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441 (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No. 163543

Seq. ID LIB3177-064-P1-K1-E3

Method BLASTX NCBI GI g1172872 BLAST score 532 2.0e-54E value Match length 103

% identity

NCBI Description CYSTEINE PROTEINASE RD19A PRECURSOR >gi 541856 pir JN0718

drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_

(D13042) thiol protease [Arabidopsis thaliana]

>gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No. 163544

Seq. ID LIB3177-064-P1-K1-E4

Method BLASTX NCBI GI g4512615 BLAST score 52 E value 9.0e-34

Match length 83 -% identity 78

NCBI Description (AC004793) Strong similarity to gb_X59970 3-isopropylmalate dehydrogenase (IMDH) from Brassica napus. EST gb_F14478

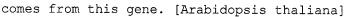
Method

NCBI GI

BLASTN

g4539331





```
Seq. No.
                    163545
Seq. ID
                    LIB3177-064-P1-K1-E5
Method
                    BLASTX
NCBI GI
                    g132102
BLAST score
                    752
E value
                    3.0e-80
Match length
                    145
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
                    (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2
                    ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.\overline{1.1.39}) small chain
                    B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_
                    (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                    thaliana]
Seq. No.
                    163546
Seq. ID
                    LIB3177-064-P1-K1-E6
Method
                    BLASTX
NCBI GI
                    q121902
BLAST score
                    422
E value
                    2.0e-41
Match length
                   136
% identity
                    68
NCBI Description HISTONE H1.1 >gi_1070594_pir__HSMU11 histone H1.1 -
                    Arabidopsis thaliana >gi 16317 emb CAA44314 (X62458)
                   Histone H1 [Arabidopsis thaliana]
Seq. No.
                   163547
Seq. ID
                   LIB3177-064-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   q541858
BLAST score
                   48
E value
                   8.0e-42
Match length
                   89
% identity
                    99
                   endoxyloglucan transferase - Arabidopsis thaliana
NCBI Description
                   >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
transferase [Arabidopsis thaliana] >gi_4063757 (AC005561)
                    endo-xyloglucan transferase [Arabidopsis thaliana]
Seq. No.
                   163548
Seq. ID
                   LIB3177-064-P1-K1-F10
Method
                   BLASTN
NCBI GI
                   g2062153
BLAST score
                   49
E value
                   2.0e-18
                   73
Match length
% identity
NCBI Description
                   Arabidopsis thaliana chromosome III BAC T02004 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163549
Seq. ID
                   LIB3177-064-P1-K1-F11
```



```
BLAST score
                   173
E value
                   2.0e-92
Match length
                   392
% identity
                  96
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13
                  (ESSA project)
                  163550
Seq. No.
Seq. ID
                  LIB3177-064-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2143227
BLAST score
                  167
E value
                  3.0e-12
Match length
                  46
% identity
                  74
NCBI Description (Y13356) glyoxysomal isocitrate lyase [Brassica napus]
Seq. No.
                  163551
Seq. ID
                  LIB3177-064-P1-K1-F2
Method
                  BLASTN
NCBI GI
                  q4468801
BLAST score
                  141
E value
                  1.0e-73
Match length
                  212
% identity
                  98
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17
                  (ESSA project)
Seq. No.
                  163552
Seq. ID
                  LIB3177-064-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g4467099
BLAST score
                  389
E value
                  5.0e-38
Match length
                  75
% identity
                  100
                  (AL035538) glycine hydroxymethyltransferase like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  163553
Seq. ID
                  LIB3177-064-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  g3449334
BLAST score
                  117
E value
                  3.0e-59
Match length
                  230
% identity
                  98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MYH9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163554
Seq. ID
                  LIB3177-064-P1-K1-F7
```

Method BLASTX NCBI GI g3286693 BLAST score 632 E value 3.0e-66 127 Match length



% identity 100 NCBI Description (Y15433) 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II [Arabidopsis thaliana] Seq. No. 163555 Seq. ID LIB3177-064-P1-K1-F8 Method BLASTN NCBI GI q4159705 BLAST score 20 E value 2.4e-01 Match length 176 % identity 93 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MGD8, complete sequence Seq. No. 163556 Seq. ID LIB3177-064-P1-K1-F9 Method BLASTN NCBI GI g4741959 BLAST score 96 E value 6.0e-47Match length 150 % identity 91 NCBI Description Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete Seq. No. 163557 Seq. ID LIB3177-064-P1-K1-G10 Method BLASTX NCBI GI q4455251 BLAST score 482 E value 1.0e-48 Match length 140 % identity 69 NCBI Description (AL035523) magnesium-protoporphyrin IX methyltransferase-like protein [Arabidopsis thaliana] Seq. No. 163558 Seq. ID LIB3177-064-P1-K1-G11 Method BLASTX NCBI GI g282865 BLAST score 311 E value 6.0e-29 Match length 73 % identity 82 NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana] Seq. No. 163559

Seq. ID LIB3177-064-P1-K1-G12

Method BLASTN NCBI GI g4589445 64

BLAST score



E value 3.0e-28 Match length 80 % identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWL2, complete sequence

Seq. No. 163560

Seq. ID LIB3177-064-P1-K1-G2

Method BLASTN
NCBI GI g3510341
BLAST score 149
E value 1.0e-78
Match length 161
% identity 37

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MFC16, complete sequence [Arabidopsis thaliana]

Seq. No. 163561

Seq. ID LIB3177-064-P1-K1-G3

Method BLASTX
NCBI GI g115767
BLAST score 645
E value 1.0e-67
Match length 140
% identity 90

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 163562

Seq. ID LIB3177-064-P1-K1-G4

Method BLASTX
NCBI GI g2271485
BLAST score 525
E value 8.0e-54
Match length 105
% identity 99

NCBI Description (AF009647) arginine decarboxylase [Arabidopsis thaliana]

>gi_3096940_emb_CAA18850.1_ (AL023094) arginine

decarboxylase SPE2 [Arabidopsis thaliana]

Seq. No. 163563

Seq. ID LIB3177-064-P1-K1-G6

Method BLASTN
NCBI GI g259446
BLAST score 158
E value 1.0e-83
Match length 177
% identity 100

NCBI Description glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana,

C24, mRNA, 680 nt]

Seq. No. 163564



Seq. ID LIB3177-064-P1-K1-G7

Method BLASTX
NCBI GI g4584523
BLAST score 307
E value 2.0e-28
Match length 61
% identity 98

NCBI Description (AL049607) putative protein [Arabidopsis thaliana]

Seq. No. 163565

Seq. ID LIB3177-064-P1-K1-G8

Method BLASTX
NCBI GI g4454037
BLAST score 726
E value 3.0e-77
Match length 139
% identity 96

NCBI Description (AL035394) putative major latex protein [Arabidopsis

thaliana]

Seq. No. 163566

Seq. ID LIB3177-064-P1-K1-G9

Method BLASTN
NCBI GI g4063737
BLAST score 68
E value 5.0e-30
Match length 96
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC F24D13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 163567

Seq. ID LIB3177-064-P1-K1-H10

Method BLASTN
NCBI GI g438448
BLAST score 65
E value 2.0e-28
Match length 101
% identity 91

NCBI Description Arabidopsis thaliana carbonic anhydrase (ca180) mRNA,

complete cds

Seq. No. 163568

Seq. ID LIB3177-064-P1-K1-H12

Method BLASTX
NCBI GI g4455210
BLAST score 557
E value 3.0e-57
Match length 127
% identity 83

NCBI Description (AL035440) putative aspartate-tRNA ligase [Arabidopsis

thaliana]

Seq. No. 163569

Seq. ID LIB3177-064-P1-K1-H3

Method BLASTX NCBI GI g397555



```
BLAST score
                   164
E value
                   2.0e-23
Match length
                   74
% identity
                   71
NCBI Description (X61664) photosystem I psaH protein [Nicotiana sylvestris]
Seq. No.
                   163570
Seq. ID
                  LIB3177-064-P1-K1-H4
Method
                  BLASTX
NCBI GI
                   g4741948
BLAST score
                   755
E value
                  2.0e-80
Match length
                  142
% identity
                  100
NCBI Description (AF134124) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                  163571
                  LIB3177-064-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115470
BLAST score
                  308
E value
                  3.0e-28
Match length
                  133
                  51
% identity
NCBI Description
                  CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
                  DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase
                   (EC 4.2.1.1) precursor - Arabidopsis thaliana
                  >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase
                   [Arabidopsis thaliana]
Seq. No.
                  163572
                  LIB3177-064-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1769905
BLAST score
                  303
E value
                  9.0e-28
Match length
                  99
% identity
                  62
NCBI Description (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                  [Arabidopsis thaliana]
Seq. No.
                  163573
Seq. ID
                  LIB3177-064-P1-K1-H8
Method
                  BLASTX
                  q4587527
                  167
                  3.0e-12
                  66
```

NCBI GI BLAST score E value Match length % identity 56

(AC007060) Strong similarity to F19I3.2 gi_3033375 putative NCBI Description

berberine bridge enzyme from Arabidopsis thaliana BAC

gb AC004238

Seq. No. 163574

Seq. ID LIB3177-064-P1-K1-H9

Method BLASTX NCBI GI g4204285



BLAST score 357 E value 6.0e-34 Match length 133 % identity 52

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 163575

Seq. ID LIB3177-065-P1-K1-A1

Method BLASTX
NCBI GI g544134
BLAST score 140
E value 7.0e-50
Match length 119
% identity 88

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR

>gi_99720_pir__S22863 hypothetical protein - Arabidopsis
thaliana >gi 421844_pir__A46260 RecA functional analog

DRT100 - Arabidopsis thaliana (fragment)

Seq. No. 163576

Seq. ID LIB3177-065-P1-K1-A10

Method BLASTN
NCBI GI g2618602
BLAST score 108
E value 7.0e-54
Match length 108
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 163577

Seq. ID LIB3177-065-P1-K1-A11

Method BLASTX
NCBI GI g4557229
BLAST score 174
E value 1.0e-12
Match length 69
% identity 43

NCBI Description angio-associated, migratory cell protein

>gi_3121739_sp_Q13685_AAMP_HUMAN_ANGIO-ASSOCIATED_MIGRATORY

CELL PROTEIN >gi_2134759_pir__ I39383 angio-associated migratory cell protein - human >gi_870803 (M95627) angio-associated migratory cell protein [Homo sapiens]

Seq. No. 163578

Seq. ID LIB3177-065-P1-K1-A12

Method BLASTX
NCBI GI g1145697
BLAST score 631
E value 4.0e-66
Match length 129
% identity 71

NCBI Description (U39485) delta tonoplast integral protein [Arabidopsis

thaliana]

Seq. No. 163579



```
Seq. ID
                   LIB3177-065-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   g3395441
BLAST score
                   219
E value
                   9.0e-18
Match length
                   62
% identity
                   58
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                  163580
Seq. ID
                  LIB3177-065-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g1363489
BLAST score
                  751
E value
                  4.0e-80
Match length
                  143
% identity
                  95
NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                  thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
Seq. No.
                  163581
Seq. ID
                  LIB3177-065-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g2894596
BLAST score
                  468
E value
                  6.0e-47
Match length
                  107
% identity
                  85
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
                  163582
Seq. No.
Seq. ID
                  LIB3177-065-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g2342684
BLAST score
                  497
E value
                  2.0e-50
Match length
                  123
% identity
NCBI Description (AC000106) F7G19.14 [Arabidopsis thaliana]
Seq. No.
                  163583
Seq. ID
                  LIB3177-065-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g135467
BLAST score
                  296
E value
                  6.0e-27
Match length
                  69
% identity
                  100
                  TUBULIN BETA-4 CHAIN >gi 2129546_pir__S68122 beta-tubulin 4
NCBI Description
```

- Arabidopsis thaliana $>\overline{g}i_1^{166640}$ (M $\overline{21}415$) beta-tubulin

[Arabidopsis thaliana]

Seq. No. 163584

Seq. ID LIB3177-065-P1-K1-A9

Method BLASTX NCBI GI g1703446



BLAST score 194 E value 2.0e-15 54 Match length 76 % identity

NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)

>gi 1076292 pir__S53127 asparaginase - Arabidopsis thaliana >gi_735918_emb CAA84367 (Z34884) asparaginase [Arabidopsis

thaliana]

163585 Seq. No.

Seq. ID LIB3177-065-P1-K1-B1

Method BLASTX NCBI GI g115783 BLAST score 557 E value 2.0e-57 Match length 107 % identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 163586

LIB3177-065-P1-K1-B10 Seq. ID

Method BLASTN NCBI GI g2737904 BLAST score 67 E value 1.0e-29 Match length 79

% identity 96

NCBI Description Arabidopsis thaliana retrotransposon TSCL mRNA sequence

Seq. No. 163587

Seq. ID LIB3177-065-P1-K1-B12

Method BLASTN NCBI GI g2245031 BLAST score 298 E value 1.0e-167 Match length 318

% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 163588

Seq. ID LIB3177-065-P1-K1-B2

Method BLASTN NCBI GI g2191126 BLAST score 318 E value 1.0e-179 Match length 334 % identity 99

NCBI Description Arabidopsis thaliana BAC IG002N01

Seq. No. 163589

Seq. ID LIB3177-065-P1-K1-B3

Method BLASTX NCBI GI g2119848



BLAST score 500 E value 9.0e-51Match length 95 % identity 97

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 -

Arabidopsis thaliana >gi 16366 emb CAA45789 (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi 3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi 3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]

Seq. No. 163590

LIB3177-065-P1-K1-B4 Seq. ID

Method BLASTX NCBI GI q1708313 390 BLAST score 5.0e-38 E value 79 Match length 100 % identity

NCBI Description HEAT SHOCK PROTEIN 81-3 (HSP81-3) >qi 999396 bbs 163637

(S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis

thaliana]

Seq. No. 163591

Seq. ID LIB3177-065-P1-K1-B5

Method BLASTX NCBI GI q115767 BLAST score 488 E value 2.0e-49 Match length 101 93 % identity

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603 pir A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 163592

Seq. ID LIB3177-065-P1-K1-B6

Method BLASTX NCBI GI g1363489 BLAST score 137 E value 9.0e-09 Match length 35 77 % identity

NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis

thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside

glucohydrolase [Arabidopsis thaliana]

Seq. No. 163593

Seq. ID LIB3177-065-P1-K1-B7

Method BLASTX



NCBI GI g4220457 BLAST score 493 E value 5.0e-50Match length 112 % identity 38

NCBI Description (AC006216) Similar to gi 3413714 T19L18.21 putative myrosinase-binding protein from Arabidopsis thaliana BAC

gb AC004747. EST gb_N96478 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 163594

Seq. ID LIB3177-065-P1-K1-C1

Method BLASTX NCBI GI g140508 BLAST score 308 E value 8.0e-29 Match length 65 % identity 88

NCBI Description PROBABLE INTRON MATURASE >gi 99852 pir S07168 probable

maturase, 63K - white mustard chloroplast

>gi_12220_emb_CAA28509 (X04826) ycf14 (AA1-324) [Sinapis

alba]

Seq. No. 163595

Seq. ID LIB3177-065-P1-K1-C10

Method BLASTN NCBI GI q4741961 BLAST score 216 E value 1.0e-118 Match length 238

% identity 98

NCBI Description Arabidopsis thaliana PsbS protein (PsbS) mRNA, complete cds

Seq. No. 163596

Seq. ID LIB3177-065-P1-K1-C11

Method BLASTX NCBI GI g1488255 BLAST score 346 E value 1.0e-32 Match length 90 % identity 69

NCBI Description (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]

>gi 2961381 emb_CAA18128 (AL022141) ferulate-5-hydroxylase

(FAH1) [Arabidopsis thaliana] >gi_3925365 (AF068574)

ferulate-5-hydroxylase [Arabidopsis thaliana]

Seq. No. 163597

Seq. ID LIB3177-065-P1-K1-C12

Method BLASTN NCBI GI q4662609 BLAST score 76 E value 5.0e-35 Match length 159 % identity

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F10A5,

complete sequence



```
Seq. No.
                    163598
Seq. ID
                   LIB3177-065-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g3286693
BLAST score
                   573
E value
                   2.0e-59
Match length
                   118
% identity
NCBI Description
                   (Y15433) 33 kDa polypeptide of oxygen-evolving complex
                    (OEC) in photosystem II [Arabidopsis thaliana]
Seq. No.
                   163599
Seq. ID
                   LIB3177-065-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g115767
BLAST score
                   589
E value
                   3.0e-61
Match length
                   116
% identity
                   98
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                   a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541 (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   163600
Seq. ID
                   LIB3177-065-P1-K1-C7
Method
                   BLASTN
NCBI GI
                   q2760165
BLAST score
                   209
E value
                   1.0e-114
Match length
                   275
% identity
                   99
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163601
Seq. ID
                   LIB3177-065-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g131211
BLAST score
                   176
E value
                   4.0e-13
Match length
                   36
% identity
                   94
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT IX (PSI-J)
                   >gi_1363533_pir__S58571 photosystem I protein psaJ - maize chloroplast >gi_552734 (J04502) ORF42 [Zea mays]
                   >gi_902241_emb_CAA60305_ (X86563) psaJ [Zea mays]
```

Seq. ID LIB3177-065-P1-K1-C9

Method BLASTX
NCBI GI g1514639
BLAST score 86
E value 3.0e-17



```
Match length
                   62
% identity
NCBI Description (X85181) alpha-glucan phosphorylase [Spinacia oleracea]
Seq. No.
                   163603
                  LIB3177-065-P1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                  g3355472
BLAST score
                  152
E value
                   2.0e-10
Match length
                  41
% identity
                   66
NCBI Description (AC004218) disease resistance response protein (206-d) like
                   [Arabidopsis thaliana]
Seq. No.
                  163604
Seq. ID
                  LIB3177-065-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g4220514
BLAST score
                  83
E value
                  4.0e-09
Match length
                  54
% identity
                  61
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  163605
Seq. ID
                  LIB3177-065-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g3236248
BLAST score
                  304
E value
                  6.0e-28
Match length
                  88
% identity
                  70
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
                  163606
Seq. ID
                  LIB3177-065-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g1703220
BLAST score
                  441
E value
                  1.0e-43
Match length
                  141
% identity
                  57
NCBI Description AIG2 PROTEIN >gi 1127806 (U40857) AIG2 [Arabidopsis
                  thaliana]
Seq. No.
                  163607
Seq. ID
                  LIB3177-065-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g227070
BLAST score
                  165
E value
                  1.0e-11
Match length
                  42
% identity
                  71
NCBI Description ribosomal protein CS-S5 [Spinacia oleracea]
```



Seq. ID LIB3177-065-P1-K1-D5 Method BLASTN NCBI GI q2264317 BLAST score 212 E value 1.0e-116 Match length 399 % identity 94 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana] Seq. No. 163609 Seq. ID LIB3177-065-P1-K1-D6 Method BLASTN NCBI GI g3282170 BLAST score 59 E value 8.0e-25 Match length 71 % identity 96 NCBI Description Arabidopsis thaliana chromosome 1 BAC F8K4 sequence, complete sequence [Arabidopsis thaliana] Seq. No. 163610 Seq. ID LIB3177-065-P1-K1-D7 Method BLASTX NCBI GI q1055161 BLAST score 159 E value 1.0e-10 Match length 151 % identity 32 NCBI Description (U40029) similar to human 100 kDa coactivator (U22055) [Caenorhabditis elegans] Seq. No. 163611 Seq. ID LIB3177-065-P1-K1-D8 Method BLASTX NCBI GI g115783 BLAST score 42 E value 3.0e-58 Match length 123 % identity 95 CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description (CAB-140) (LHCP) >gi_16376_emb CAA27543 (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana] Seq. No. 163612 Seq. ID LIB3177-065-P1-K1-D9 Method BLASTN

NCBI GI q2760165 BLAST score 89 E value 2.0e-42Match length

293 % identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MAC9, complete sequence [Arabidopsis thaliana]

Seq. No. 163613

% identity

81



```
Seq. ID
                   LIB3177-065-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g1169235
BLAST score
                   139
E value
                   1.0e-08
Match length
                   74
% identity
                   46
NCBI Description
                   DIAMINOPIMELATE DECARBOXYLASE (DAP DECARBOXYLASE)
                   >gi_1073995_pir__B64089 diaminopimelate decarboxylase (dap
                   decarboxylase) (lysA) homolog - Haemophilus influenzae
                   (strain Rd KW20) >gi_1573731 (U32756) diaminopimelate
                   decarboxylase (lysA) [Haemophilus influenzae Rd]
Seq. No.
                   163614
Seq. ID
                   LIB3177-065-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   q2129630
BLAST score
                   436
E value
                   3.0e-43
Match length
                   86
% identity
                   94
NCBI Description lamin - Arabidopsis thaliana >gi 1262754 emb CAA65750
                   (X97023) lamin [Arabidopsis thaliana] >gi 33\overline{9}5760 (U7\overline{7}721)
                   unknown [Arabidopsis thaliana]
Seq. No.
                   163615
Seq. ID
                   LIB3177-065-P1-K1-E11
Method
                   BLASTN
NCBI GI
                   q3212102
BLAST score
                   122
E value
                   2.0e-62
Match length
                   170
% identity
                   95
NCBI Description Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   163616
Seq. ID
                   LIB3177-065-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   q2062167
BLAST score
                   543
E value
                   9.0e-56
Match length
                   105
% identity
                   97
NCBI Description
                  (ACO01645) Proline-rich protein APG isolog [Arabidopsis
                   thaliana]
Seq. No.
                   163617
Seq. ID
                  LIB3177-065-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q2924772
BLAST score
                  153
E value
                  2.0e-10
Match length
                  37
```

NCBI Description (AC002334) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                   163618
Seq. ID
                   LIB3177-065-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   g2650351
BLAST score
                   154
E value
                   2.0e-10
Match length
                   78
                   40
% identity
NCBI Description
                  (AE001085) 3-hydroxyacyl-CoA dehydrogenase (hbd-2)
                   [Archaeoglobus fulgidus]
                   163619
Seq. No.
Seq. ID
                  LIB3177-065-P1-K1-E4
Method
                  BLASTX
NCBI GI
                   g3334123
BLAST score
                   395
E value
                   1.0e-38
Match length
                   99
                   85
% identity
NCBI Description
                  ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi 1655480 dbj BAA13599 (D88374) gamma subunit of
                  mitochondrial F1-ATPase [Arabidopsis thaliana] >qi 2924787
                   (AC002334) mitochondrial F1-ATPase, gamma subunit
                   [Arabidopsis thaliana]
Seq. No.
                  163620
Seq. ID
                  LIB3177-065-P1-K1-E7
Method
                  BLASTN
                  g16206
NCBI GI
BLAST score
                  75
E value
                  8.0e-35
Match length
                  75
% identity
                  100
NCBI Description A.thaliana Cab mRNA for photossystem I chlorophyll
                  A/B-binding protein
Seq. No.
                  163621
Seq. ID
                  LIB3177-065-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q4567303
BLAST score
                  604
E value
                  6.0e - 63
Match length
                  114
% identity
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]
Seq. No.
                  163622
Seq. ID
                  LIB3177-065-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  g2244788
BLAST score
                  104
E value
```

Match length 204 % identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

1.0e-51

Seq. ID

Method

NCBI GI



```
Seq. No.
                   163623
Seq. ID
                   LIB3177-065-P1-K1-F1
Method
                   BLASTN
NCBI GI
                   g3687221
BLAST score
                   58
                   2.0e-24
E value
                   86
Match length
                   92
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F6F22 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163624
Seq. ID
                   LIB3177-065-P1-K1-F10
Method
                   BLASTN
NCBI GI
                   g4589444
BLAST score
                   58
E value
                   3.0e-24
Match length
                   140
                   95
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MWF20, complete sequence
                   163625
Seq. No.
Seq. ID
                  LIB3177-065-P1-K1-F4
Method
                  BLASTX
NCBI GI
                   g4006879
                   581
BLAST score
E value
                   2.0e-60
Match length
                  113
                   100
% identity
NCBI Description
                  (Z99707) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  163626
Seq. ID
                  LIB3177-065-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q3953473
BLAST score
                  452
E value
                  4.0e-45
Match length
                  117
% identity
NCBI Description
                  (AC002328) F2202.18 [Arabidopsis thaliana]
Seq. No.
                  163627
Seq. ID
                  LIB3177-065-P1-K1-F7
Method
                  BLASTN
NCBI GI
                  g4589428
BLAST score
                  265
E value
                  1.0e-147
Match length
                  289
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFH8, complete sequence
Seq. No.
                  163628
```

21845

LIB3177-065-P1-K1-F8

BLASTX

g4567235



```
BLAST score
                   231
E value
                   2.0e-19
Match length
                   59
                   80
% identity
                   (AC007119) putative phosphatidylinositol/phophatidylcholine
NCBI Description
                   transfer protein [Arabidopsis thaliana]
Seq. No.
                   163629
Seq. ID
                   LIB3177-065-P1-K1-F9
Method
                   BLASTN
NCBI GI
                   g3869074
BLAST score
                   46
E value
                   5.0e-17
Match length
                   79
% identity
                   93
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
NCBI Description
                  MMI9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163630
Seq. ID
                   LIB3177-065-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g231564
BLAST score
                   390
E value
                   4.0e-38
Match length
                   81
% identity
                   94
NCBI Description PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 2 PRECURSOR
                   (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 2) (DAHP
                  SYNTHETASE 2) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE
                   SYNTHASE 2) >gi_166690 (M74820)
                   3-deoxy-D-arabino-heptulosonate 7-phosphate synthase
                   [Arabidopsis thaliana]
Seq. No.
                  163631
Seq. ID
                  LIB3177-065-P1-K1-G10
Method
                  BLASTN
NCBI GI
                  q786465
BLAST score
                  90
E value
                  2.0e-43
Match length
                  133
% identity
                  93
NCBI Description
                  sedoheptulose-1,7-bisphosphatase [Arabidopsis thaliana,
                  C24, Genomic, 2747 nt]
Seq. No.
                  163632
Seq. ID
                  LIB3177-065-P1-K1-G11
Method
                  BLASTN
                  q4454022
                  32
                  3.0e-09
```

NCBI GI BLAST score E value Match length 36 % identity

Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 NCBI Description

(ESSAII project)

Seq. No. 163633

Seq. ID LIB3177-065-P1-K1-G12



Method BLASTX
NCBI GI g119975
BLAST score 474
E value 7.0e-48
Match length 98
% identity 98

NCBI Description FERREDOXIN PRECURSOR >gi 99692 pir S09979 ferredoxin

[2Fe-2S] precursor - Arabidopsis thaliana

>gi_16437_emb_CAA35754 (X51370) ferredoxin precursor
[Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A

[Arabidopsis thaliana]

Seq. No. 163634

Seq. ID LIB3177-065-P1-K1-G2

Method BLASTN
NCBI GI g2894591
BLAST score 137
E value 3.0e-71
Match length 213
% identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21

(ESSAII project)

Seq. No. 163635

Seq. ID LIB3177-065-P1-K1-G3

Method BLASTX
NCBI GI g1621268
BLAST score 524
E value 2.0e-53
Match length 137
% identity 69

NCBI Description (Z81012) unknown [Ricinus communis]

Seq. No. 163636

Seq. ID LIB3177-065-P1-K1-G4

Method BLASTN
NCBI GI g4063735
BLAST score 107
E value 3.0e-53
Match length 171
% identity 92

NCBI Description Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5

cM, complete sequence [Arabidopsis thaliana]

Seq. No. 163637

Seq. ID LIB3177-065-P1-K1-G5

Method BLASTX
NCBI GI g3785997
BLAST score 225
E value 4.0e-19
Match length 66
% identity 74

MCBI Description (AC005499) putative annexin [Arabidopsis thaliana]

Seq. No. 163638

Seq. ID LIB3177-065-P1-K1-G6

Method BLASTX



```
NCBI GI
                   q2244969
BLAST score
                   182
E value
                   5.0e-14
Match length
                   47
% identity
                   77
                   (Z97340) hypothetical gene [Arabidopsis thaliana]
NCBI Description
                   >gi_3549643_emb_CAA06433_ (AJ005196) receiver-like protein
                   5 [Arabidopsis thaliana]
Seq. No.
                   163639
Seq. ID
                   LIB3177-065-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g3869253
BLAST score
                   749
E value
                   7.0e-80
Match length
                   147
% identity
                   100
NCBI Description
                  (U39288) ferredoxin-dependent glutamate synthase precursor
                   [Arabidopsis thaliana]
Seq. No.
                   163640
Seq. ID
                  LIB3177-065-P1-K1-G9
Method
                  BLASTX
NCBI GI
                   q3157937
BLAST score
                   327
E value
                   7.0e-31
Match length
                   69
% identity
                   99
NCBI Description
                  (AC002131) Identical to aspartic proteinase cDNA gb_U51036
                   from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158,
                   gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269,
                   gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591,
                   gb_AA728734, gb
Seq. No.
                   163641
Seq. ID
                  LIB3177-065-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g4454036
BLAST score
                  165
E value
                  7.0e-12
Match length
                  71
% identity
                   48
NCBI Description
                  (AL035394) putative major latex protein [Arabidopsis
                  thaliana]
Seq. No.
                  163642
Seq. ID
                  LIB3177-065-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  q4159704
BLAST score
                  314
E value
                  1.0e-176
Match length
                  322
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
```

MCB17, complete sequence



```
LIB3177-065-P1-K1-H12
Seq. ID
Method
                  BLASTX
                  g2244881
NCBI GI
BLAST score
                  512
E value
                  4.0e-52
                  103
Match length
                  61
% identity
NCBI Description
                  (Z97338) PDR5-like ABC transporter [Arabidopsis thaliana]
Seq. No.
                  163644
                  LIB3177-065-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2559012
BLAST score
                  361
E value
                  1.0e-34
Match length
                  92
                  76
% identity
NCBI Description
                  (AF026293) chaperonin containing t-complex polypeptide 1,
                  beta subunit; CCT-beta [Homo sapiens] >gi 4090929
                   (AF026166) chaperonin-containing TCP-1 beta subunit homolog
                   [Homo sapiens]
Seq. No.
                  163645
                  LIB3177-065-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  618
                  2.0e-64
E value
Match length
                  116
                  100
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi_16376_emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  163646
Seq. ID
                  LIB3177-065-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q3892714
BLAST score
                  611
E value
                  1.0e-63
Match length
                  130
% identity
NCBI Description
                  (AL033545) trehalose-6-phosphate phosphatase-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  163647
Seq. ID
                  LIB3177-065-P1-K1-H7
Method
                  BLASTN
NCBI GI
                  q1769904
BLAST score
                  120
E value
                  3.0e-61
```

Match length 14497 % identity

NCBI Description A.thaliana psbP gene

Seq. No. 163648



```
Seq. ID
                   LIB3177-065-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   q1854386
BLAST score
                   362
E value
                   7.0e-35
Match length
                   88
% identity
                   77
NCBI Description
                  (AB001375) similar to soluble NSF attachment protein [Vitis
                  vinifera]
Seq. No.
                   163649
Seq. ID
                  LIB3177-066-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q2851508
BLAST score
                  162
E value
                   1.0e-11
Match length
                   32
% identity
                   97
NCBI Description
                  60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to
                   ribosomal protein L21 (gb L38826). ESTs
                   gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis
                  thaliana] >gi_3482935 (AC003970) Putative ribosomal protein
                  L21 [Arabidopsis thaliana]
Seq. No.
                  163650
Seq. ID
                  LIB3177-066-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  q4454037
BLAST score
                  387
E value
                   4.0e-38
Match length
                  69
% identity
                  99
                  (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  163651
Seq. ID
                  LIB3177-066-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2864617
BLAST score
                  428
E value
                  2.0e-42
Match length
                  124
% identity
                  73
NCBI Description
                  (AL021811) H+-transporting ATP synthase chain9 - like
                  protein [Arabidopsis thaliana]
Seq. No.
                  163652
Seq. ID
                  LIB3177-066-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q3763921
BLAST score
                  200
E value
                  1.0e-15
Match length
                  58
% identity
NCBI Description
                 (AC004450) putative pirin protein [Arabidopsis thaliana]
```



```
Seq. ID
                   LIB3177-066-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   g2398527
BLAST score
                   177
E value
                   2.0e-13
Match length
                   36
% identity
                   97
NCBI Description (Y13723) Transcription factor [Arabidopsis thaliana]
Seq. No.
                   163654
Seq. ID
                   LIB3177-066-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   q2072393
BLAST score
                   215
E value
                   7.0e-18
Match length
                   51
                   86
% identity
NCBI Description
                  (U29168) similar to human Xeroderma pigmentosum group B DNA
                   repair protein, Swiss-Prot Accession Number P19447
                   [Arabidopsis thaliana]
Seq. No.
                   163655
Seq. ID
                   LIB3177-066-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   g4263712
BLAST score
                   335
E value
                   2.0e-31
Match length
                   96
                   73
% identity
NCBI Description
                  (AC006223) putative ribosomal protein S12 [Arabidopsis
                   thalianal
Seq. No.
                   163656
Seq. ID
                   LIB3177-066-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   q136636
BLAST score
                   366
E value
                   5.0e-35
Match length
                   70
% identity
                   100
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
                   LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                   >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 -
                   Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin
                   Conjugating Enzyme (E.C.\overline{6}.3.2.1\overline{9}) >\overline{gi}29\overline{8}1894_pdb 2AAK
                   Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                   >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis
                   thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
                   [Arabidopsis thaliana]
Seq. No.
                   163657
Seq. ID
                   LIB3177-066-P1-K1-B11
Method
                  BLASTN
```

NCBI GI g4512690
BLAST score 239
E value 1.0e-132
Match length 433



```
% identity
                   100
NCBI Description Arabidopsis thaliana chromosome II BAC F11A3 genomic
                  sequence, complete sequence
Seq. No.
                 . 163658
Seq. ID
                  LIB3177-066-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g2062161
BLAST score
                  463
E value
                  3.0e-47
Match length
                  102
                  52
% identity
NCBI Description
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                  163659
Seq. ID
                  LIB3177-066-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  q2182287
BLAST score
                  73
E value
                  4.0e-33
Match length
                  129
                  89
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T7N9,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  163660
Seq. ID
                  LIB3177-066-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  g2980757
BLAST score
                  140
E value
                  3.0e-73
Match length
                  152
% identity
                  98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18
                  (ESSAII project)
Seq. No.
                  163661
Seq. ID
                  LIB3177-066-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q1402878
BLAST score
                  263
E value
                  3.0e-23
Match length
                  93
% identity
                  58
NCBI Description (X98130) unknown [Arabidopsis thaliana]
Seq. No.
                  163662
                  LIB3177-066-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1619300
BLAST score
                  182
```

Method BLASTX
NCBI GI g161930
BLAST score 182
E value 8.0e-14
Match length 51
% identity 71

NCBI Description (X95269) LRR protein [Lycopersicon esculentum]

Seq. ID

163668

LIB3177-066-P1-K1-C8



```
Seq. No.
                   163663
Seq. ID
                   LIB3177-066-P1-K1-C12
Method
                   BLASTN
NCBI GI
                   q2335089
BLAST score
                   102
E value
                   3.0e-50
Match length
                   126
% identity
                   95
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T11A7 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163664
Seq. ID
                   LIB3177-066-P1-K1-C2
Method
                   BLASTN
NCBI GI
                   g16473
BLAST score
                   375
E value
                   0.0e + 00
Match length
                   403
% identity
                   98
NCBI Description Arabidopsis thaliana 25S-18S ribosomal DNA spacer
Seq. No.
                   163665
Seq. ID
                   LIB3177-066-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   g2499535
BLAST score
                   352
E value
                   9.0e-34
Match length
                   82
% identity
                   80
                   2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi_595681
NCBI Description
                   (U13238) 2-oxoglutarate/malate translocator [Spinacia
                   oleracea]
Seq. No.
                   163666
Seq. ID
                   LIB3177-066-P1-K1-C5
Method
                   BLASTN
NCBI GI
                   q2264316
BLAST score
                   86
                   2.0e-40
E value
Match length
                   427
% identity
                   39
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRO11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163667
Seq. ID
                  LIB3177-066-P1-K1-C7
Method
                  BLASTN
NCBI GI
                   q3540210
BLAST score
                   41
E value
                   2.0e-14
                  77
Match length
% identity
                   90
                  Arabidopsis thaliana chromosome I BAC F5A8 genomic
NCBI Description
```

21853

sequence, complete sequence [Arabidopsis thaliana]



```
Method
                   BLASTX
NCBI GI
                   q4741940
BLAST score
                   260
E value
                   3.0e-23
Match length
                   73
% identity
                   67
NCBI Description (AF134120) Lhca2 protein [Arabidopsis thaliana]
Seq. No.
                  163669
Seq. ID
                  LIB3177-066-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g1346520
BLAST score
                  413
E value
                  2.0e-40
Match length
                  102
% identity
                  79
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
                  ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
                  >gi_790978_emb_CAA56590_ (X80362) S-adenosyl-L-methionine
                  synthetase [Brassica juncea]
Seq. No.
                  163670
Seq. ID
                  LIB3177-066-P1-K1-D1
Method
                  BLASTN
NCBI GI
                  g1167960
BLAST score
                  37
E value
                  3.0e-11
Match length
                  343
% identity
                  36
NCBI Description Arabidopsis thaliana extensin (atExt1) gene, complete cds
Seq. No.
                  163671
Seq. ID
                  LIB3177-066-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q945039
BLAST score
                  138
E value
                  7.0e-09
Match length
                  36
% identity
                  72
NCBI Description (U25027) phosphatidylinositol-specific phospholipase C
                  [Glycine max]
Seq. No.
                  163672
Seq. ID
                  LIB3177-066-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g2062161
BLAST score
                  319
E value
                  2.0e-29
Match length
                  61
% identity
                  51
NCBI Description
                 (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                  163673
```

Seq. ID LIB3177-066-P1-K1-D3

Method BLASTX NCBI GI g2062161



```
BLAST score
                  348
                  8.0e-33
E value
Match length
                  71
% identity
                  48
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  163674
Seq. No.
                  LIB3177-066-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2497733
BLAST score
                  203
E value
                  2.0e-16
Match length
                  53
% identity
                  65
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)
NCBI Description
                  >gi 1177796 (M80567) non-specific lipid transfer protein
                  [Arabidopsis thaliana] >gi 3786018 (AC005499) unknown
                  protein [Arabidopsis thaliana]
                  163675
Seq. No.
                  LIB3177-066-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g841208
BLAST score
                  309
E value
                  3.0e-28
Match length
                  128
% identity
                  55
NCBI Description (U18995) trypsin inhibitor propeptide [Brassica oleracea]
Seq. No.
                  163676
                  LIB3177-066-P1-K1-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2642427
BLAST score
                  58
E value
                  8.0e-24
Match length
                  94
                  90
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC T20D16 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163677
Seq. ID
                  LIB3177-066-P1-K1-D8
Method
                  BLASTN
NCBI GI
                  g17681
BLAST score
                  52
E value
                  3.0e-20
Match length
                  208
% identity
                  88
NCBI Description A.thaliana mRNA for Wilm's tumor suppressor homologue
Seq. No.
                  163678
```

Seq. ID LIB3177-066-P1-K1-D9

Method BLASTX
NCBI GI g4510373
BLAST score 323
E value 7.0e-30



Match length 126 % identity 56

NCBI Description (AC007017) putative harpin-induced protein [Arabidopsis

thaliana]

Seq. No. 163679

Seq. ID LIB3177-066-P1-K1-E1

Method BLASTX
NCBI GI g2369714
BLAST score 237
E value 2.0e-20
Match length 51
% identity 96

NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 163680

Seq. ID LIB3177-066-P1-K1-E10

Method BLASTX
NCBI GI g1169278
BLAST score 178
E value 2.0e-13
Match length 44
% identity 86

NCBI Description DEHYDRIN ERD14 >gi 556474 dbj BAA04569 (D17715) ERD14

protein [Arabidopsis thaliana]

Seq. No. 163681

Seq. ID LIB3177-066-P1-K1-E11

Method BLASTX
NCBI GI g131398
BLAST score 337
E value 7.0e-32
Match length 70
% identity 99

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb_N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400

come from this gene. [Arabidopsis

Seq. No. 163682

Seq. ID LIB3177-066-P1-K1-E2

Method BLASTX
NCBI GI g2924779
BLAST score 626
E value 2.0e-65
Match length 149
% identity 86

NCBI Description (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis

thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA

thiolase [Arabidopsis thaliana]



163683

LIB3177-066-P1-K1-E3

Seq. No.

Seq. ID

```
Method
                  BLASTX
NCBI GI
                  g2791423
BLAST score
                  192
E value
                  1.0e-14
Match length
                  69
                  54
% identity
NCBI Description (AL021185) bcp [Mycobacterium tuberculosis]
Seq. No.
                  163684
Seq. ID
                  LIB3177-066-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  q2129636
BLAST score
                  724
E value
                  6.0e-77
Match length
                  153
% identity
                  91
NCBI Description lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase
                  [Arabidopsis thaliana]
Seq. No.
                  163685
Seq. ID
                  LIB3177-066-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g2129636
BLAST score
                  278
E value
                  1.0e-24
Match length
                  86
% identity
                  65
NCBI Description lipase - Arabidopsis thaliana >gi 1145627 (U38916) lipase
                  [Arabidopsis thaliana]
Seq. No.
                  163686
Seq. ID
                  LIB3177-066-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2462077
BLAST score
                  397
E value
                  7.0e-39
Match length
                  82
% identity
                  95
NCBI Description (Y11871) Oxal protein [Arabidopsis thaliana]
Seq. No.
                  163687
Seq. ID
                  LIB3177-066-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g2791423
BLAST score
                  207
E value
                  3.0e-16
Match length
                  71
% identity
                  55
NCBI Description (AL021185) bcp [Mycobacterium tuberculosis]
Seq. No.
                  163688
                  LIB3177-066-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462825
```



BLAST score 609 E value 2.0e-63 Match length 131 % identity 92

NCBI Description (AF000657) contains Procite 'RNP1' putative RNA-binding

region [Arabidopsis thaliana]

Seq. No. 163689

Seq. ID LIB3177-066-P1-K1-F1

Method BLASTX
NCBI GI 94469408
BLAST score 260
E value 1.0e-22
Match length 63
% identity 81

NCBI Description (AF116527) MADS box protein FLOWERING LOCUS F [Arabidopsis

thaliana] >gi 4469410 gb AAD21249 (AF116528) MADS box

protein FLOWERING LOCUS F [Arabidopsis thaliana]

Seq. No. 163690

Seq. ID LIB3177-066-P1-K1-F10

Method BLASTX
NCBI GI g1066163
BLAST score 244
E value 1.0e-20
Match length 48
% identity 98

NCBI Description (X93015) glyoxysomal beta-ketoacyl-thiolase [Brassica

napus]

Seq. No. 163691

Seq. ID LIB3177-066-P1-K1-F12

Method BLASTX
NCBI GI g731284
BLAST score 198
E value 3.0e-15
Match length 126
% identity 37

NCBI Description HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION

>gi_1077482_pir__S51971 probable membrane protein YAL048c -

yeast (Saccharomyces cerevisiae) >gi_595536 (U12980)

Yal048cp [Saccharomyces cerevisiae]

Seq. No. 163692

Seq. ID LIB3177-066-P1-K1-F2

Method BLASTN
NCBI GI g16470
BLAST score 171
E value 2.0e-91
Match length 187
% identity 98

NCBI Description Arabidopsis thaliana mRNA for rubisco activase

Seq. No. 163693

Seq. ID LIB3177-066-P1-K1-F3

Method BLASTX NCBI GI g135391



```
BLAST score
                  447
E value
                  1.0e-44
Match length
                  83
% identity
                  100
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_71583_pir__UBMUAM tubulin alpha-1
                  chain - Arabidopsis thaliana >gi 166896 (M21414)
                  alpha-1-tubulin [Arabidopsis thaliana]
Seq. No.
                  163694
                  LIB3177-066-P1-K1-F4
Seq. ID
Method
                  BLASTX
                  g2160166
NCBI GI
BLAST score
                  372
E value
                  6.0e-36
Match length
                  101
% identity
                  70
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                  163695
Seq. ID
                  LIB3177-066-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g399013
BLAST score
                  593
E value
                  1.0e-61
Match length
                  120
% identity
                  98
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                  >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                  thaliana (fragment) >gi 16175 emb CAA46518 (X65549)
                  adenylate translocator [Arabidopsis thaliana]
                  >gi 445607 prf 1909354A adenylate translocator
                  [Arabidopsis thaliana]
Seq. No.
                  163696
Seq. ID
                  LIB3177-066-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g2764941
BLAST score
                  600
E value
                  2.0e-62
Match length
                  105
% identity
                  100
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
Seq. No.
                  163697
```

Seq. ID LIB3177-066-P1-K1-F8

Method BLASTX
NCBI GI g2088654
BLAST score 484
E value 6.0e-49
Match length 114
% identity 86

NCBI Description (AF002109) 60S acidic ribosomal protein PO isolog

[Arabidopsis thaliana]



Seq. ID LIB3177-066-P1-K1-F9

Method BLASTN
NCBI GI g1946354
BLAST score 163
E value 8.0e-87
Match length 221
% identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T06B20 genomic

sequence, complete sequence

Seq. No. 163699

Seq. ID LIB3177-066-P1-K1-G11

Method BLASTX
NCBI GI g3193292
BLAST score 355
E value 6.0e-34
Match length 80
% identity 88

NCBI Description (AF069298) similar to ATPases associated with various

cellular activites (Pfam: AAA.hmm, score: 230.91)

[Arabidopsis thaliana]

Seq. No. 163700

Seq. ID LIB3177-066-P1-K1-G2

Method BLASTX
NCBI GI g3335371
BLAST score 449
E value 5.0e-45
Match length 96
% identity 91

NCBI Description (AC003028) putative ethylene-inducible protein [Arabidopsis

thaliana]

Seq. No. 163701

Seq. ID LIB3177-066-P1-K1-G4

Method BLASTX
NCBI GI g4586249
BLAST score 328
E value 2.0e-30
Match length 140
% identity 44

NCBI Description (AL049640) putative pollen surface protein [Arabidopsis

thaliana]

Seq. No. 163702

Seq. ID LIB3177-066-P1-K1-G5

Method BLASTX
NCBI GI g131398
BLAST score 311
E value 2.0e-28
Match length 89
% identity 71

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor
- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
photosystem II 10 kDa polypeptide [Arabidopsis thaliana]



>gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No. 163703

LIB3177-066-P1-K1-G6 Seq. ID

Method BLASTN NCBI GI g1167960 BLAST score 42 E value 3.0e-14Match length 244 % identity 30

NCBI Description Arabidopsis thaliana extensin (atExt1) gene, complete cds

163704 Seq. No.

LIB3177-066-P1-K1-G7 Seq. ID

Method BLASTX NCBI GI g2244798 BLAST score 324 E value 4.0e-30 Match length 62

100 % identity

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 163705

Seq. ID LIB3177-066-P1-K1-G8

Method BLASTX g1769905 NCBI GI BLAST score 455 E value 2.0e-45 Match length 129 % identity 69

NCBI Description (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)

[Arabidopsis thaliana]

Seq. No. 163706

Seq. ID LIB3177-066-P1-K1-G9

Method BLASTX NCBI GI q4741960 BLAST score 155 E value 1.0e-46 Match length 139 % identity

NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 163707

Seq. ID LIB3177-066-P1-K1-H10

Method BLASTN NCBI GI g3413696 BLAST score 297 E value 1.0e-166 Match length 305 % identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T19L18 genomic

sequence, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                  163708
Seq. ID
                  LIB3177-066-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g282865
BLAST score
                  323
E value
                  3.0e-30
Match length
                  71
                  85
% identity
NCBI Description
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
                  >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi 166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi_4678304 emb CAB41095.1 (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  163709
                  LIB3177-066-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170373
BLAST score
                  668
E value
                  3.0e-70
Match length
                  130
                  98
% identity
NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi 1072473 pir S46302
                  heat shock cognate protein 70-1 - Arabidopsis thaliana
                  >gi_397482_emb_CAA52684 (X74604) heat shock protein 70
                  cognate [Arabidopsis thaliana]
Seq. No.
                  163710
Seq. ID
                  LIB3177-066-P1-K1-H4
Method
                  BLASTN
                  g2062153
NCBI GI
BLAST score
                  102
E value
                  3.0e-50
Match length
                  110
% identity
                  98
NCBI Description Arabidopsis thaliana chromosome III BAC T02004 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163711
Seq. ID
                  LIB3177-066-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  g4006885
BLAST score
                  58
E value
                  3.0e-24
Match length
                  58
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
```

Seq. ID LIB3177-066-P1-K1-H6

fragment No

Method BLASTN
NCBI GI g469113
BLAST score 345
E value 0.0e+00

Match length

NCBI Description

% identity

65

100



```
Match length
                   357
                   99
% identity
NCBI Description A.thaliana (Columbia) Dr4 mRNA
Seq. No.
                   163713
                   LIB3177-066-P1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4510402
BLAST score
                   80
                   1.2e-01
E value
Match length
                   109
% identity
                   45
NCBI Description
                  (AC006587) putative AP2 domain [Arabidopsis thaliana]
Seq. No.
                   163714
Seq. ID
                   LIB3177-066-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   q1702987
BLAST score
                   529
                   4.0e-54
E value
Match length
                   107
% identity
                   100
NCBI Description
                  14-3-3-LIKE PROTEIN GF14 PHI >gi 1493805 (L09111) GF14
                  protein phi chain [Arabidopsis thaliana] >gi 2232146
                   (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis
                   thaliana]
Seq. No.
                   163715
Seq. ID
                  LIB3177-066-P1-K1-H9
Method
                  BLASTN
NCBI GI
                  q4559375
BLAST score
                   151
E value
                   2.0e-79
Match length
                   245
                   99
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F11C10 genomic
                   sequence, complete sequence
Seq. No.
                  163716
Seq. ID
                  LIB3177-067-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  g469113
BLAST score
                   393
E value
                   0.0e + 00
Match length
                   424
                   99
% identity
NCBI Description A.thaliana (Columbia) Dr4 mRNA
Seq. No.
                   163717
Seq. ID
                  LIB3177-067-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q2832683
BLAST score
                   332
E value
                   6.0e - 31
```

21863

(AL021712) putative protein [Arabidopsis thaliana]



Seq. ID LIB3177-067-P1-K1-A2

Method BLASTN
NCBI GI g4589950
BLAST score 210
E value 1.0e-114
Match length 393
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC T28P16 genomic

sequence, complete sequence

Seq. No. 163719

Seq. ID LIB3177-067-P1-K1-A3

Method BLASTN
NCBI GI g4199934
BLAST score 196
E value 1.0e-106
Match length 216
% identity 35

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 163720

Seq. ID LIB3177-067-P1-K1-A4

Method BLASTX
NCBI GI g4522012
BLAST score 302
E value 2.0e-27
Match length 90
% identity 61

NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 163721

Seq. ID LIB3177-067-P1-K1-A5

Method BLASTX
NCBI GI g886116
BLAST score 651
E value 2.0e-68
Match length 125
% identity 98

NCBI Description (U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473

(AF051338) xyloglucan endotransglycosylase related protein

[Arabidopsis thaliana]

Seq. No. 163722

Seq. ID LIB3177-067-P1-K1-A7

Method BLASTN
NCBI GI g16363
BLAST score 40
E value 3.0e-13
Match length 103
% identity 87

NCBI Description A.thaliana Lhb1B2 gene for photosystem II chlorophyll a/b

binding protein

Seq. No. 163723



Seq. ID LIB3177-067-P1-K1-A8

Method BLASTX NCBI GI g2493810 BLAST score 237 E value 4.0e-20 Match length 43 % identity 98

NCBI Description COPROPORPHYRINOGEN III OXIDASE PRECURSOR

(COPROPORPHYRINOGENASE) (COPROGEN OXIDASE)

>gi 1213067 emb CAA58038 (X82831) coproporphyrinogen

oxidase [Nicotiana tabacum]

Seq. No. 163724

LIB3177-067-P1-K1-B1 Seq. ID

Method BLASTX NCBI GI g3287862 BLAST score 339 E value 5.0e-32 Match length 63 % identity 95

NCBI Description PUTATIVE TRYPSIN INHIBITOR T01024.27 PRECURSOR >qi 2289007

(AC002335) trypsin inhibitor 2 precursor isolog

[Arabidopsis thaliana]

Seq. No. 163725

LIB3177-067-P1-K1-B10 Seq. ID

Method BLASTN NCBI GI q4580744 BLAST score 133 E value 4.0e-69 Match length 137 % identity 56

NCBI Description Sequence of BAC F15I1 from Arabidopsis thaliana chromosome

1, complete sequence

Seq. No. 163726

Seq. ID LIB3177-067-P1-K1-B11

Method BLASTX g549010 NCBI GI BLAST score 701 E value 3.0e-74Match length 137 % identity 100

NCBI Description EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG)

>gi_322554_pir__S31328 omnipotent suppressor protein SUP1

homolog (clone G18) - Arabidopsis thaliana

>gi_16514_emb_CAA49172_ (X69375) similar to yeast
omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis

thaliana] >gi_1495249_emb_CAA66118_ (X97486) eRF1-3

[Arabidopsis thaliana]

Seq. No. 163727

Seq. ID LIB3177-067-P1-K1-B12

Method BLASTN



NCBI GI g4406805 BLAST score 281 E value 1.0e-157 Match length 429 % identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 163728

Seq. ID LIB3177-067-P1-K1-B2

Method BLASTN
NCBI GI g4199934
BLAST score 91
E value 4.0e-44
Match length 103
% identity 74

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 163729

Seq. ID LIB3177-067-P1-K1-B4

Method BLASTX
NCBI GI g132110
BLAST score 356
E value 4.0e-34
Match length 76
% identity 93

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_(X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 163730

Seq. ID LIB3177-067-P1-K1-B5

Method BLASTN
NCBI GI g4544381
BLAST score 75
E value 5.0e-34
Match length 79
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F16F14 genomic

sequence, complete sequence

Seq. No. 163731

Seq. ID LIB3177-067-P1-K1-B6

Method BLASTX
NCBI GI 94337175
BLAST score 520
E value 5.0e-53
Match length 131
% identity 79

NCBI Description (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,

gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

% identity

NCBI Description

98

(ESSAII project)



```
Seq. No.
                    163732
                    LIB3177-067-P1-K1-B8
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1778141
 BLAST score
                    528
                    5.0e-54
 E value
                    138
 Match length
                    78
 % identity
 NCBI Description
                   (U66321) phosphate/phosphoenolpyruvate translocator
                   precursor; PPT [Arabidopsis thaliana]
 Seq. No.
                    163733
 Seq. ID
                    LIB3177-067-P1-K1-B9
 Method
                    BLASTX
 NCBI GI
                    g1170089
 BLAST score
                    307
                    1.0e-28
 E value
                    63
 Match length
                    98
 % identity
                   GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)
 NCBI Description
                    >gi_481822 pir S39542 probable glutathione transferase (EC
                    2.5.1.18) (clone ERD13) - Arabidopsis thaliana
                    >gi 497789 dbj BAA04554 (D17673) glutathione S-transferase
                    [Arabidopsis thaliana] >gi 3201614 (AC004669) glutathione
                    S-transferase [Arabidopsis thaliana]
 Seq. No.
                    163734
                   LIB3177-067-P1-K1-C1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g4741960
 BLAST score
                    620
. E value
                    1.0e-64
 Match length
                    140
 % identity
                    85
 NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
 Seq. No.
                   163735
 Seq. ID
                   LIB3177-067-P1-K1-C11
 Method
                   BLASTX
 NCBI GI
                    g2435406
 BLAST score
                    183
 E value
                    7.0e-14
 Match length
                    49
                    65
 % identity
 NCBI Description (U83490) thaumatin-like protein [Arabidopsis thaliana]
 Seq. No.
                   163736
 Seq. ID
                   LIB3177-067-P1-K1-C12
 Method
                   BLASTN
 NCBI GI
                   q4455348
 BLAST score
                    140
 E value
                    5.0e-73
                   263
 Match length
```

21867

Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8



```
Seq. No.
                   163737
Seq. ID
                   LIB3177-067-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g3355480
BLAST score
                   242
E value
                   2.0e-20
Match length
                   79
% identity
                   56
                   (AC004218) Medicago nodulin N21-like protein [Arabidopsis
NCBI Description
Seq. No.
                   163738
                   LIB3177-067-P1-K1-C3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2618720
BLAST score
                   132
E value
                   3.0e-68
Match length
                   172
% identity
                   95
NCBI Description Arabidopsis thaliana early auxin-induced (IAA16) mRNA,
                   complete cds
Seq. No.
                   163739
                   LIB3177-067-P1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4056503
BLAST score
                   169
                   3.0e-12
E value
Match length
                   36
                   92
% identity
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.
                   163740
                   LIB3177-067-P1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1621268
BLAST score
                   373
E value
                   5.0e-36
                   107
Match length
% identity
                   68
NCBI Description (Z81012) unknown [Ricinus communis]
                   163741
Seq. No.
Seq. ID
                   LIB3177-067-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g113026
BLAST score
                   614
E value
                   5.0e-64
Match length
                   132
                   89
% identity
NCBI Description
                   ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
                   >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape
>gi_255220_bbs_112862 isocitrate lyase, threo-D
                   S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica
```

21868

napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482)
isocitrate lyase [Brassica napus] >gi 447142 prf 1913424A



isocitrate lyase [Brassica napus]

```
Seq. No.
                  163742
                  LIB3177-067-P1-K1-C9
Seq. ID
Method
                  BLASTN
                  g2264318
NCBI GI
BLAST score
                  138
                   8.0e-72
E value
Match length
                   226
                   92
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUP24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163743
                  LIB3177-067-P1-K1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3201608
BLAST score
                  130
E value
                   4.0e-67
                  157
Match length
                   96
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F7F1 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  163744
Seq. No.
                  LIB3177-067-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567268
BLAST score
                  261
                   4.0e-23
E value
Match length
                   60
                   93
% identity
NCBI Description
                  (AC006841) putative fructose biphosphate aldolase
                   [Arabidopsis thaliana]
Seq. No.
                  163745
Seq. ID
                  LIB3177-067-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  q3522932
BLAST score
                  165
E value
                  8.0e-88
Match length
                  277
% identity
                   97
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F14M4 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163746
Seq. ID
                  LIB3177-067-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q1732570
BLAST score
                  137
E value
                  5.0e-09
                  59
Match length
% identity
```

Seq. No. 163747

NCBI Description

(U72153) beta-glucosidase [Arabidopsis thaliana]



```
Seq. ID
                  LIB3177-067-P1-K1-D5
Method
                  BLASTN
NCBI GI
                   q4309683
                  98
BLAST score
E value
                   4.0e-48
Match length
                  154
                  92
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T31J12 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  163748
                  LIB3177-067-P1-K1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3883125
BLAST score
                  297
                  1.0e-166
E value
Match length
                  388
% identity
                  95
NCBI Description
                  Arabidopsis thaliana arabinogalactan-protein (AGP4) mRNA,
                  complete cds
Seq. No.
                  163749
Seq. ID
                  LIB3177-067-P1-K1-D8
Method
                  BLASTN
NCBI GI
                  g3929648
BLAST score
                  177
E value
                   4.0e-95
Match length
                  205
                  97
% identity
NCBI Description Arabidopsis thaliana mRNA for mitochondrial NAD-dependent
                  malate dehydrogenase
Seq. No.
                  163750
                  LIB3177-067-P1-K1-E1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3299824
BLAST score
                  43
E value
                  7.0e-16
Match length
                  61
% identity
                  92
NCBI Description
                  Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,
                  near 17 cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163751
Seq. ID
                  LIB3177-067-P1-K1-E10
                  BLASTN
                  g16470
                  98
```

Method NCBI GI BLAST score 3.0e-48E value Match length 118 % identity 96

NCBI Description Arabidopsis thaliana mRNA for rubisco activase

Seq. No. 163752

Seq. ID LIB3177-067-P1-K1-E12

Method BLASTN NCBI GI g950098



```
BLAST score
                  163
E value
                  8.0e-87
Match length
                  187
% identity
                  97
NCBI Description
```

Arabidopsis thaliana gibberellin-regulated (GASA4) mRNA, complete cds

163753 Seq. No.

Seq. ID LIB3177-067-P1-K1-E2

Method BLASTX NCBI GI g115767 BLAST score 650 E value 3.0e-68 Match length 127 % identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 163754

Seq. ID LIB3177-067-P1-K1-E5

Method BLASTN NCBI GI q47594 BLAST score 85 4.0e-40 E value Match length 161 % identity 91

NCBI Description Synechocystis sp. ndhE gene (partial), psaC gene for

photosystem I iron-sulfur protein and ndhD-like ORF

Seq. No. 163755

Seq. ID LIB3177-067-P1-K1-E6

Method BLASTN NCBI GI q3283056 BLAST score 48 E value 3.0e-18 Match length 127

NCBI Description Arabidopsis thaliana one helix protein (OHP) mRNA, complete

cds

84

Seq. No. 163756

% identity

Seq. ID LIB3177-067-P1-K1-E7

Method BLASTX NCBI GI g132110 BLAST score 393 E value 2.0e-38 79 Match length % identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir_RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_



(X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No. 163757

Seq. ID LIB3177-067-P1-K1-E8

Method BLASTX
NCBI GI g115783
BLAST score 601
E value 1.0e-62
Match length 114
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 163758

Seq. ID LIB3177-067-P1-K1-E9

Method BLASTN
NCBI GI g343376
BLAST score 32
E value 9.0e-09
Match length 59
% identity 90

NCBI Description Spinach rps4 gene encoding ribosomal protein S4, complete

cds, with Thr-tRNA and Ser-tRNA genes

Seq. No. 163759

Seq. ID LIB3177-067-P1-K1-F1

Method BLASTX
NCBI GI g1170089
BLAST score 260
E value 3.0e-23
Match length 64
% identity 86

NCBI Description GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)

>gi_481822_pir__S39542 probable glutathione transferase (EC

2.5.1.18) (clone ERD13) - Arabidopsis thaliana

>gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase
[Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione

S-transferase [Arabidopsis thaliana]

Seq. No. 163760

Seq. ID LIB3177-067-P1-K1-F11

Method BLASTX
NCBI GI g4454470
BLAST score 344
E value 1.0e-32
Match length 109
% identity 68

NCBI Description (AC006234) putative sugar transporter [Arabidopsis

thaliana]

Seq. No. 163761

Seq. ID LIB3177-067-P1-K1-F12

Method BLASTX NCBI GI g2499327



BLAST score 365 E value 6.0e-35 Match length 118 % identity 64

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_1084345_pir__S52286 NADH

dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_643090_emb_CAA58887.1_ (X84078) NADH dehydrogenase

[Arabidopsis thaliana]

Seq. No. 163762

Seq. ID LIB3177-067-P1-K1-F3

Method BLASTX
NCBI GI 94454479
BLAST score 356
E value 7.0e-34
Match length 74
% identity 97

NCBI Description (AC006234) putative riboflavin synthase alpha chain

[Arabidopsis thaliana]

Seq. No. 163763

Seq. ID LIB3177-067-P1-K1-F4

Method BLASTX
NCBI GI g1175013
BLAST score 221
E value 1.0e-18
Match length 42
% identity 98

NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084

plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic

protein 2a [Arabidopsis thaliana]

Seq. No. 163764

Seq. ID LIB3177-067-P1-K1-F9

Method BLASTX
NCBI GI g3157937
BLAST score 259
E value 1.0e-22
Match length 60
% identity 82

NCBI Description (AC002131) Identical to aspartic proteinase cDNA gb_U51036

from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591,

gb_AA728734, gb

Seq. No. 163765

Seq. ID LIB3177-067-P1-K1-G1

Method BLASTX
NCBI GI g2493052
BLAST score 373
E value 5.0e-36
Match length 70
% identity 100

NCBI Description ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL

% identity

NCBI Description

58

melanogaster]



>gi_1655486_dbj_BAA13602_ (D88377) epsilon subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

163766 Seq. No. LIB3177-067-P1-K1-G11 Seq. ID Method BLASTX NCBI GI q4538903 BLAST score 139 E value 9.0e-09 72 Match length % identity 43 NCBI Description (AL049482) putative protein [Arabidopsis thaliana] Seq. No. 163767 Seq. ID LIB3177-067-P1-K1-G12 Method BLASTX q3695383 NCBI GI BLAST score 250 1.0e-21 E value Match length 61 % identity 82 (AF096370) similar to inorganic pyrophosphatase (Pfam: NCBI Description PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis thaliana] 163768 Seq. No. LIB3177-067-P1-K1-G2 Seq. ID Method BLASTX NCBI GI g2911042 BLAST score 357 2.0e-34 E value 72 Match length % identity 100 (AL021961) Phosphoglycerate dehydrogenase - like protein NCBI Description [Arabidopsis thaliana] Seq. No. 163769 LIB3177-067-P1-K1-G3 Seq. ID Method BLASTX NCBI GI q4490732 BLAST score 567 E value 1.0e-58 Match length 120 % identity (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like NCBI Description protein [Arabidopsis thaliana] Seq. No. 163770 Seq. ID LIB3177-067-P1-K1-G4 Method BLASTX q2815905 NCBI GI BLAST score 290 E value 4.0e-26 Match length 98

21874

(AF043734) Pros45 proteosome subunit homolog [Drosophila



```
Seq. No.
                  163771
                  LIB3177-067-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2851508
BLAST score
                  49
                  2.0e-32
E value
                  70
Match length
                  100
% identity
                 60S RIBOSOMAL PROTEIN L21 >gi 2160162 (AC000132) Similar to
NCBI Description
                  ribosomal protein L21 (gb_L38826). ESTs
                  gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis
                  thaliana] >gi 3482935 (AC003970) Putative ribosomal protein
                  L21 [Arabidopsis thaliana]
Seq. No.
                  163772
                  LIB3177-067-P1-K1-G6
Seq. ID
Method
                  BLASTN
                  q3063438
NCBI GI
                  82
BLAST score
                  3.0e-38
E value
Match length
                  160
% identity
                  88
NCBI Description Complete sequence of Arabidopsis F22013, complete sequence
                  [Arabidopsis thaliana]
Seq. No.
                  163773
                  LIB3177-067-P1-K1-G8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q132102
BLAST score
                  414
E value
                  7.0e-41
Match length
                  88
                  94
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
                  (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  163774
Seq. ID
                  LIB3177-067-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g2129640
BLAST score
                  389
E value
                  4.0e-38
Match length
                  84
% identity
                  magnesium chelatase chain - Arabidopsis thaliana
NCBI Description
                  >gi 1154627 emb CAA92802 (Z68495) magnesium chelatase
                  subunit [Arabidopsis thaliana]
```

Seq. No. 163775

Seq. ID LIB3177-067-P1-K1-H10

Method BLASTX NCBI GI g115767



BLAST score 624 E value 2.0e-66 Match length 132 % identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 163776

Seq. ID LIB3177-067-P1-K1-H11

Method BLASTX
NCBI GI g1732570
BLAST score 277
E value 3.0e-25
Match length 73
% identity 77

NCBI Description (U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No. 163777

Seq. ID LIB3177-067-P1-K1-H12

Method BLASTX
NCBI GI g115385
BLAST score 687
E value 1.0e-72
Match length 131
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 163778

Seq. ID LIB3177-067-P1-K1-H2

Method BLASTN
NCBI GI g3212846
BLAST score 200
E value 1.0e-109
Match length 244
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 163779

Seq. ID LIB3177-067-P1-K1-H3

Method BLASTN
NCBI GI 94056476
BLAST score 113
E value 7.0e-57
Match length 194
% identity 95

NCBI Description Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

sequence, complete sequence [Alabidopsis thailana]

Seq. No. 163780



Seq. ID LIB3177-067-P1-K1-H5 Method BLASTX

100

Method BLASTX
NCBI GI g2119848
BLAST score 513
E value 2.0e-52
Match length 95

% identity

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B1 -

Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein

[Arabidopsis thaliana]

Seq. No. 163781

Seq. ID LIB3177-067-P1-K1-H6

Method BLASTX
NCBI GI g421836
BLAST score 142
E value 2.0e-09
Match length 30
% identity 97

NCBI Description G-box-binding factor GF14 - Arabidopsis thaliana >gi 553040

(M96855) GF14 [Arabidopsis thaliana]

Seq. No. 163782

Seq. ID LIB3177-067-P1-K1-H8

Method BLASTN
NCBI GI g3172156
BLAST score 189
E value 1.0e-102
Match length 336
% identity 98

NCBI Description Arabidopsis thaliana chromosome 1 BAC T22J18 sequence,

complete sequence [Arabidopsis thaliana]

Seq. No. 163783

Seq. ID LIB3177-067-P1-K1-H9

Method BLASTX
NCBI GI g131381
BLAST score 597
E value 3.0e-62
Match length 117
% identity 98

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi_99745_pir__S11852

photosystem II oxygen-evolving complex protein 1 precursor - Arabidopsis thaliana >gi_22571_emb_CAA36675_ (X52428) 33

kDa oxygen-evolving protein [Arabidopsis thaliana]

Seq. No. 163784

Seq. ID LIB3177-068-P1-K1-A10

Method BLASTX NCBI GI g3157944



BLAST score 561 E value 8.0e-58 Match length 109 % identity 98

NCBI Description (AC002131) Very strong similarity to aminomethyltransferase

precursor gb_U79769 from Mesembryanthemum crystallinum.

ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773,

gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123

come from this ge

Seq. No. 163785

Seq. ID LIB3177-068-P1-K1-A11

Method BLASTX
NCBI GI g118514
BLAST score 179
E value 2.0e-25
Match length 88
% identity 65

NCBI Description TURGOR-RESPONSIVE PROTEIN 26G >gi 100051 pir S11863

aldehyde dehydrogenase homolog - garden pea

>gi_20681_emb_CAA38243_ (X54359) 508 aa peptide [Pisum

sativum]

Seq. No. 163786

Seq. ID LIB3177-068-P1-K1-A12

Method BLASTN
NCBI GI g3421079
BLAST score 353
E value 0.0e+00
Match length 357
% identity 100

NCBI Description Arabidopsis thaliana 20S proteasome subunit PAD1 (PAD1)

mRNA, complete cds

Seq. No. 163787

Seq. ID LIB3177-068-P1-K1-A2

Method BLASTX
NCBI GI g132110
BLAST score 582
E value 2.0e-60
Match length 116
% identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 163788

Seq. ID LIB3177-068-P1-K1-A3

Method BLASTN
NCBI GI g2244829
BLAST score 228
E value 1.0e-125
Match length 404
% identity 98



```
fragment No
                  163789
Seq. No.
                  LIB3177-068-P1-K1-A4
Seq. ID
                  BLASTN
Method
                  g4756963
NCBI GI
                  372
BLAST score
                  0.0e+00
E value
                  439
Match length
                  95
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                  (ESSA project)
                  163790
Seq. No.
                  LIB3177-068-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1168201
                  502
BLAST score
                  5.0e-51
E value
                  116
Match length
% identity
                  89
                  14-3-3-LIKE PROTEIN RCI2 >gi 1076394 pir S47970 RCI1B
NCBI Description
                  protein - Arabidopsis thaliana >gi 531379 emb CAA52238
                  (X74141) RCI1B [Arabidopsis thaliana]
                  163791
Seq. No.
                  LIB3177-068-P1-K1-A6
Seq. ID
                  BLASTX
Method
                  g1732570
NCBI GI
BLAST score
                  164
E value
                  1.0e-23
                  57
Match length
                  90
% identity
NCBI Description (U72153) beta-glucosidase [Arabidopsis thaliana]
Seq. No.
                  163792
                  LIB3177-068-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2262167
BLAST score
                  435
E value
                  3.0e-43
Match length
                  94
                  88
% identity
                  (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  163793
Seq. ID
                  LIB3177-068-P1-K1-A9
Method
                  BLASTN
NCBI GI
                  g2244829
BLAST score
                  40
E value
                  3.0e-13
Match length
                  40
% identity
                  100
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
```

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

NCBI GI

E value

BLAST score

q2760169

1.0e-100

186



```
Seq. No.
                  163794
Seq. ID
                  LIB3177-068-P1-K1-B10
                  BLASTX
Method
NCBI GI
                  q131398
BLAST score
                  554
                  5.0e-57
E value
Match length
                  140
                  81
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                  >gi 72714 pir F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >gi 16447 emb CAA39441 (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >gi 3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide gb_X55970. ESTs gb Z17693, gb N37616,
                  gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
                  gb N64965, gb Z17592 and gb N65338, gb N37466 and gb T45400
                  come from this gene. [Arabidopsis
Seq. No.
                  163795
                  LIB3177-068-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2062161
BLAST score
                  588
E value
                  4.0e-61
Match length
                  128
% identity
                  53
NCBI Description
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
                  thaliana]
                  163796
Seq. No.
Seq. ID
                  LIB3177-068-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  g438448
BLAST score
                  34
                  4.0e-10
E value
Match length
                  38
% identity
                  97
NCBI Description Arabidopsis thaliana carbonic anhydrase (ca180) mRNA,
                  complete cds
                  163797
Seq. No.
Seq. ID
                  LIB3177-068-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g4741940
BLAST score
                  536
E value
                  6.0e-55
Match length
                  118
% identity
NCBI Description (AF134120) Lhca2 protein [Arabidopsis thaliana]
                  163798
Seq. No.
Seq. ID
                  LIB3177-068-P1-K1-B3
Method
                  BLASTN
```



Match length 350 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MFB13, complete sequence [Arabidopsis thaliana]

Seq. No. 163799

Seq. ID LIB3177-068-P1-K1-B4

Method BLASTX
NCBI GI g4585882
BLAST score 105
E value 9.0e-62
Match length 127
% identity 97

NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 163800

Seq. ID LIB3177-068-P1-K1-B5

Method BLASTX
NCBI GI 94454037
BLAST score 694
E value 2.0e-73
Match length 136
% identity 94

NCBI Description (AL035394) putative major latex protein [Arabidopsis

thaliana]

Seq. No. 163801

Seq. ID LIB3177-068-P1-K1-B6

Method BLASTX
NCBI GI g1628478
BLAST score 463
E value 3.0e-46
Match length 102

% identity 91

NCBI Description (X98536) variant histone H2A.Z12 [Xenopus laevis]

>gi_1685280 (U77893) histone H2A.Z variant [Xenopus laevis]
>gi_1695198_emb_CAA67148_ (X98535) variant histone H2A.Z11

[Xenopus laevis]

Seq. No. 163802

Seq. ID LIB3177-068-P1-K1-B7

Method BLASTN
NCBI GI g3985954
BLAST score 95
E value 3.0e-46
Match length 171
% identity 45

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

MRG21, complete sequence [Arabidopsis thaliana]

Seq. No. 163803

Seq. ID LIB3177-068-P1-K1-B8

Method BLASTX
NCBI GI g2129670
BLAST score 140
E value 2.0e-64



Match length 128 % identity 95 NCBI Description phosphoinositide-specific phospholipase C - Arabidopsis thaliana >gi 857374 dbj BAA09432 (D50804) phosphoinositide specific phospholipase C [Arabidopsis thaliana] Seq. No. 163804 Seq. ID LIB3177-068-P1-K1-B9 Method BLASTX NCBI GI g2828267 BLAST score 331 5.0e-31 E value 92 Match length % identity 75 NCBI Description (Y14044) geranylgeranyl reductase [Arabidopsis thaliana] Seq. No. 163805 LIB3177-068-P1-K1-C1 Seq. ID Method BLASTX NCBI GI q2829868 BLAST score 130 E value 2.0e-46117 Match length 88 % identity NCBI Description (AC002396) Unknown protein [Arabidopsis thaliana] Seq. No. 163806 LIB3177-068-P1-K1-C10 Seq. ID Method BLASTN NCBI GI g2618604 BLAST score 143 E value 1.0e-74Match length 155 98 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG13, complete sequence [Arabidopsis thaliana] Seq. No. 163807 Seq. ID LIB3177-068-P1-K1-C11 Method BLASTX NCBI GI q3859536 BLAST score 581 E value 2.0e-60 Match length 112 % identity 99 NCBI Description (AF095453) asparagine synthetase [Arabidopsis thaliana] Seq. No. 163808

Seq. ID LIB3177-068-P1-K1-C12

Method BLASTN NCBI GI q2980757

BLAST score 51 E value 7.0e-20 Match length 127 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18

(ESSAII project)



Seq. No. 163809

Seq. ID LIB3177-068-P1-K1-C2

Method BLASTN
NCBI GI g3449326
BLAST score 217
E value 1.0e-119
Match length 264
% identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19M22, complete sequence [Arabidopsis thaliana]

Seq. No. 163810

Seq. ID LIB3177-068-P1-K1-C3

Method BLASTX
NCBI GI g119143
BLAST score 278
E value 1.0e-24
Match length 54
% identity 100

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi_81606_pir__S06724 translation elongation factor eEF-1
alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
(X16430) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1369927_emb_CAA34454_ (X16431) elongation factor
1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_
(X16431) elongation factor 1-alpha [Arabidopsis thaliana]
>gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
>gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
>gi_1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]

Seq. No. 163811

Seq. ID LIB3177-068-P1-K1-C4

Method BLASTX
NCBI GI g2119846
BLAST score 440
E value 5.0e-44
Match length 92
% identity 91

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 163812

Seq. ID LIB3177-068-P1-K1-C5

Method BLASTX
NCBI GI g1710581
BLAST score 417
E value 4.0e-41
Match length 91
% identity 89

NCBI Description 60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir_S71255 ribosomal

protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_



(X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No. 163813 Seq. ID

LIB3177-068-P1-K1-C6

Method BLASTX q4539302 NCBI GI BLAST score 654 8.0e-69 E value 129 Match length 96 % identity

(AL049480) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 163814

LIB3177-068-P1-K1-C7 Seq. ID

Method BLASTX NCBI GI g4263525 BLAST score 527 8.0e-54E value Match length 125 % identity 82

(AC004044) putative photosystem I reaction center subunit NCBI Description

II precursor [Arabidopsis thaliana]

Seq. No. 163815

LIB3177-068-P1-K1-C8 Seq. ID

Method BLASTX NCBI GI g2129651 BLAST score 762 E value 2.0e-81 Match length 147 100 % identity

myosin heavy chain ATM2 - Arabidopsis thaliana (fragment) NCBI Description

>gi 499045 emb CAA84065 (Z34292) myosin [Arabidopsis

thaliana]

163816 Seq. No.

LIB3177-068-P1-K1-D10 Seq. ID

Method BLASTN NCBI GI g4559375 BLAST score 231 1.0e-127 E value 424 Match length 100 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F11C10 genomic

sequence, complete sequence

Seq. No. 163817

Seq. ID LIB3177-068-P1-K1-D11

Method BLASTX NCBI GI g2832605 BLAST score 695 E value 2.0e-73 Match length 153 % identity

(AL021633) predicted protein [Arabidopsis thaliana] NCBI Description

163818 Seq. No.



LIB3177-068-P1-K1-D2 Seq. ID Method BLASTX NCBI GI g132074 BLAST score 517 E value 7.0e-53 Match length 105 95 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain Al precursor - Arabidopsis thaliana Seq. No. 163819 Seq. ID LIB3177-068-P1-K1-D3 Method BLASTN NCBI GI g2459406 BLAST score 202 1.0e-110 E value Match length 402 99 % identity Arabidopsis thaliana chromosome II BAC F4P9 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 163820 Seq. No. LIB3177-068-P1-K1-D4 Seq. ID Method BLASTN NCBI GI g4519194 BLAST score 257 1.0e-142 E value Match length 288 97 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence 163821 Seq. No. Seq. ID LIB3177-068-P1-K1-D5 Method BLASTX g1370186 NCBI GI BLAST score 516 E value 2.0e-52 Match length 101 % identity NCBI Description (Z73942) RAB7C [Lotus japonicus] Seq. No. 163822 Seq. ID LIB3177-068-P1-K1-D6 Method BLASTX NCBI GI q4582787 BLAST score 334 E value 2.0e-31 77 Match length % identity NCBI Description (AJ012281) adenosine kinase [Zea mays]

Seq. No. 163823

Seq. ID LIB3177-068-P1-K1-D7

Method BLASTX



```
NCBI GI
                   g2911085
                   345
BLAST score
E value
                  2.0e-39
Match length
                  113
% identity
                  81
                  (AL021960) photosystem II oxygen-evolving complex protein
NCBI Description
                   3-like [Arabidopsis thaliana] >gi 3402748 emb CAA20194.1
                   (AL031187) photosystem II oxygen-evolving complex protein 3

    like [Arabidopsis thaliana]

Seq. No.
                  163824
Seq. ID
                  LIB3177-068-P1-K1-D8
Method
                  BLASTN
```

NCBI GI g4559344 BLAST score 350 E value 0.0e + 00Match length 404 % identity

Arabidopsis thaliana chromosome II BAC F27C12 genomic NCBI Description

sequence, complete sequence

Seq. No. 163825 Seq. ID LIB3177-068-P1-K1-D9 Method BLASTX NCBI GI g3023516 BLAST score 343 E value 9.0e-33 Match length 78

% identity 87

NCBI Description PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE PRECURSOR

(DXP SYNTHASE) >gi 1399261 (U27099) DEF [Arabidopsis

thaliana]

163826 Seq. No.

LIB3177-068-P1-K1-E1 Seq. ID

Method BLASTX NCBI GI g4725941 519 BLAST score E value 6.0e-53 Match length 112 % identity 86

(AL049730) putative pollen-specific protein [Arabidopsis NCBI Description

thaliana]

163827 Seq. No.

LIB3177-068-P1-K1-E10 Seq. ID

Method BLASTX NCBI GI g1175013 BLAST score 571 E value 5.0e-59 Match length 126 % identity 89

NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi 629542 pir S44084

plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]



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Seq. No.
                  163828
                  LIB3177-068-P1-K1-E11
Seq. ID
Method
                  BLASTX
                  q115783
NCBI GI
                  698
BLAST score
                  6.0e-74
E value
                  136
Match length
                  97
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  163829
Seq. No.
                  LIB3177-068-P1-K1-E12
Seq. ID
Method
                  BLASTX
                  q3286693
NCBI GI
BLAST score
                  618
                  2.0e-64
E value
                  128
Match length
% identity
                  98
                  (Y15433) 33 kDa polypeptide of oxygen-evolving complex
NCBI Description
                  (OEC) in photosystem II [Arabidopsis thaliana]
                  163830
Seq. No.
                  LIB3177-068-P1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1169601
BLAST score
                  743
                  4.0e-79
E value
                  146
Match length
                  99
% identity
                  OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 493068 (U09503) chloroplast omega-6 fatty acid
                  desaturase [Arabidopsis thaliana]
                  163831
Seq. No.
                  LIB3177-068-P1-K1-E3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4581084
BLAST score
                  280
                  1.0e-156
E value
Match length
                  332
                  99
% identity
NCBI Description Arabidopsis thaliana chromosome I BAC T30F21 genomic
                  sequence, complete sequence
                  163832
Seq. No.
                  LIB3177-068-P1-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4713943
                  98
```

BLAST score

E value 3.0e-48Match length 146 92 % identity

NCBI Description Arabidopsis thaliana chromosome 1 BAC T8K14 sequence,

complete sequence



Seq. No. 163833 Seq. ID LIB3177-068-P1-K1-E5 Method BLASTX NCBI GI q4586256 BLAST score 247 4.0e-21 E value Match length 62 % identity 81 (AL049640) probable photosystem I chain XI precursor NCBI Description [Arabidopsis thaliana] Seq. No. 163834 LIB3177-068-P1-K1-E6 Seq. ID Method BLASTN NCBI GI g3869069 BLAST score 56 E value 1.0e-22 Match length 389 87 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MEB5, complete sequence [Arabidopsis thaliana] Seq. No. 163835 LIB3177-068-P1-K1-E7 Seq. ID Method BLASTX NCBI GI g115783 BLAST score 508 E value 9.0e-52 95 Match length 100 % identity CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana] 163836 Seq. No. Seq. ID LIB3177-068-P1-K1-F1 Method BLASTX g421826 NCBI GI BLAST score 618 2.0e-64 E value 141 Match length % identity 82 chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana NCBI Description >gi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis thaliana] 163837 Seq. No.

Seq. ID LIB3177-068-P1-K1-F10

Method BLASTX q4741960 NCBI GI BLAST score 478 E value 4.0e-48 Match length 111 % identity

(AF134130) Lhcb6 protein [Arabidopsis thaliana] NCBI Description



97

% identity

NCBI Description

```
Seq. No.
                  163838
                  LIB3177-068-P1-K1-F11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4519190
                  136
BLAST score
                  2.0e-70
E value
                  464
Match length
% identity
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K6A12, complete sequence
Seq. No.
                  163839
                  LIB3177-068-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914442
BLAST score
                  518
E value
                  9.0e-53
Match length
                  140
                  74
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                  >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]
Seq. No.
                  163840
                  LIB3177-068-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1145697
BLAST score
                  514
                  2.0e-52
E value
Match length
                  106
% identity
                  53
                  (U39485) delta tonoplast integral protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  163841
Seq. ID
                  LIB3177-068-P1-K1-F4
Method
                  BLASTN
NCBI GI
                  q4206762
BLAST score
                  49
E value
                   2.0e-18
Match length
                  334
% identity
                   40
NCBI Description
                  Arabidopsis thaliana cell wall-plasma membrane linker
                  protein homolog (CWLP) mRNA, complete cds
Seq. No.
                  163842
Seq. ID
                  LIB3177-068-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  g3299824
BLAST score
                  427
E value
                  0.0e + 00
Match length
                  471
```

near 17 cM, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,

% identity

NCBI Description

97



```
Seq. No.
                  163843
Seq. ID
                  LIB3177-068-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g282865
                  670
BLAST score
                  1.0e-70
E value
Match length
                  133
                  72
% identity
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
NCBI Description
                  >gi 16207 emb CAA39534 (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi 166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi 4678304 emb CAB41095.1 (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  163844
                  LIB3177-068-P1-K1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q516248
BLAST score
                  200
                  1.0e-109
E value
Match length
                  228
% identity
                  97
NCBI Description A.thaliana gene for porphobilinogen deaminase
Seq. No.
                  163845
Seq. ID
                  LIB3177-068-P1-K1-F9
Method
                  BLASTN
NCBI GI
                  q4220635
BLAST score
                  127
E value
                  3.0e-65
Match length
                  217
% identity
                  91
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MDB19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163846
Seq. ID
                  LIB3177-068-P1-K1-G1
Method
                  BLASTX
                  g421826
NCBI GI
BLAST score
                  337
E value
                  9.0e-32
Match length
                  101
                  63
% identity
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                  >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                  thaliana]
Seq. No.
                  163847
Seq. ID
                  LIB3177-068-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  q4678268
BLAST score
                  52
E value
                  6.0e-50
Match length
                  103
```

21890

(AL049660) putative protein [Arabidopsis thaliana]



```
Seq. No. 163848
Seq. ID LIB3177-068-P1-K1-G12
Method BLASTX
NCBI GI g4539009
BLAST score 661
E value 2.0e-69
Match length 156
```

NCBI Description (AL049481) putative protein [Arabidopsis thaliana]

Seq. No. 163849

% identity

Seq. ID LIB3177-068-P1-K1-G2

76

Method BLASTX
NCBI GI g1175010
BLAST score 317
E value 1.0e-46
Match length 113

% identity 88
NCBI Description PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__S44082

plasma membrane intrinsic protein 1a - Arabidopsis thaliana >gi 472873 emb CAA53475 (X75881) plasma membrane intrinsic

protein la [Arabidopsis thaliana]

Seq. No. 163850

Seq. ID LIB3177-068-P1-K1-G4

Method BLASTX
NCBI GI g115767
BLAST score 619
E value 1.0e-64
Match length 119
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 163851

Seq. ID LIB3177-068-P1-K1-G5

Method BLASTN
NCBI GI g4589412
BLAST score 46
E value 1.0e-16
Match length 155
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F6N7, complete sequence

Seq. No. 163852

Seq. ID LIB3177-068-P1-K1-G6

Method BLASTX NCBI GI g3914442 BLAST score 424 E value 7.0e-42

E value

Match length

% identity

4.0e-25

55

95



```
Match length
                  121
% identity
                  71
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                  >gi 1916350 (U92504) PSI-H subunit [Brassica rapa]
Seq. No.
                  163853
                  LIB3177-068-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2809244
BLAST score
                  449
E value
                  1.0e-44
Match length
                  82
% identity
                  100
                  (AC002560) F21B7.13 [Arabidopsis thaliana]
NCBI Description
                  163854
Seq. No.
Seq. ID
                  LIB3177-068-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q2289010
BLAST score
                  454
                  1.0e-45
E value
                  93
Match length
                  97
% identity
NCBI Description
                  (AC002335) FKBP type peptidyl-prolyl cis-trans isomerase
                  isolog [Arabidopsis thaliana]
Seq. No.
                  163855
                  LIB3177-068-P1-K1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3337347
BLAST score
                  162
                  6.0e-86
E value
Match length
                  296
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13P17 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163856
Seq. ID
                  LIB3177-068-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  q1237123
BLAST score
                  350
E value
                  0.0e + 00
Match length
                  350
% identity
NCBI Description
                  Arabidopsis thaliana photosystem I PSI-N mRNA, nuclear gene
                  encoding chloroplast protein, complete cds
                  163857
Seq. No.
Seq. ID
                  LIB3177-068-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q4406777
BLAST score
                  282
```



```
NCBI Description
                  (AC006532) putative zinc-finger protein [Arabidopsis
                  thaliana]
                  163858
Seq. No.
Seq. ID
                  LIB3177-068-P1-K1-H12
                  BLASTX
Method
                  g2894564
NCBI GI
BLAST score
                  127
E value
                  9.0e-28
                  66
Match length
                  98
% identity
                 (AL021890) putative protein [Arabidopsis thaliana]
NCBI Description
                  163859
Seq. No.
Seq. ID
                  LIB3177-068-P1-K1-H2
                  BLASTN
Method
NCBI GI
                  g3298610
BLAST score
                  127
E value
                  2.0e-65
Match length
                  135
                  99
% identity
NCBI Description Arabidopsis thaliana BAC T2H3
                  163860
Seq. No.
Seq. ID
                  LIB3177-068-P1-K1-H3
                  BLASTN
Method
NCBI GI
                  g2760829
BLAST score
                  297
E value
                  1.0e-166
Match length
                  324
% identity
                  97
NCBI Description Arabidopsis thaliana chromosome II BAC F18A8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163861
Seq. ID
                  LIB3177-068-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2146741
BLAST score
                  630
E value
                  5.0e-66
Match length
                  119
% identity
                  100
NCBI Description
                  isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) -
                  Arabidopsis thaliana >qi 1293565 (U49259) isopentenyl
                  diphosphate:dimethylallyl diphosphate isomerase
                  [Arabidopsis thaliana]
Seq. No.
                  163862
                  LIB3177-068-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1477480
BLAST score
                  739
E value
                  1.0e-78
Match length
                  145
                  52
% identity
                  (U40341) carbamoyl phosphate synthetase large chain
NCBI Description
```

21893

[Arabidopsis thaliana]



```
Seq. No.
                  163863
Seq. ID
                  LIB3177-068-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q3449041
BLAST score
                  486
                  3.0e-49
E value
Match length
                  90
                  97
% identity
NCBI Description
                  (U73462) carbonic anhydrase [Arabidopsis thaliana]
                  163864
Seq. No.
Seq. ID
                  LIB3177-068-P1-K1-H7
                  BLASTN
Method
NCBI GI
                  q4159706
BLAST score
                  104
E value
                  7.0e-52
Match length
                  127
% identity
                  100
NCBI Description
                 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGL6, complete sequence
Seq. No.
                  163865
Seq. ID
                  LIB3177-068-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g166835
BLAST score
                  525
E value
                  7.0e-54
Match length
                  100
                  100
% identity
                  (M86720) ribulose bisphosphate carboxylase/oxygenase
NCBI Description
                  activase [Arabidopsis thaliana] >gi 2642170 (AC003000)
                  Rubisco activase [Arabidopsis thaliana]
                  163866
Seq. No.
                  LIB3177-068-P1-K1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g600388
BLAST score
                  285
                  1.0e-159
E value
                  306
Match length
% identity
                  98
NCBI Description A.thaliana UbcAT3 mRNA for ubiquitin conjugating enzyme E2
                  163867
Seq. No.
                  LIB3177-069-P1-K1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4519192
BLAST score
                  258
```

E value 1.0e-143 Match length 262 100 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MBK21, complete sequence

Seq. No. 163868

LIB3177-069-P1-K1-A11 Seq. ID



```
Method
                  BLASTN
NCBI GI
                  g2244788
                  52
BLAST score
                  1.0e-20
E value
                  71
Match length
                  96
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  163869
Seq. No.
                  LIB3177-069-P1-K1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1916349
                  121
BLAST score
E value
                  1.0e-61
Match length
                  227
                  90
% identity
NCBI Description Brassica rapa PSI-H subunit (psaH) mRNA, complete cds
                  163870
Seq. No.
                  LIB3177-069-P1-K1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2982285
                  350
BLAST score
                  4.0e-33
E value
                  69
Match length
                  80
% identity
                  (AF051227) GASA5-like protein [Picea mariana]
NCBI Description
Seq. No.
                  163871
                  LIB3177-069-P1-K1-A3
Seq. ID
                  BLASTX
Method
                  g4587564
NCBI GI
                  186
BLAST score
                  2.0e-14
E value
                  37
Match length
% identity
                  97
NCBI Description
                  (AC006550) Strong similarity to gb_X14017 photosystem I
                  reaction centre subunit II precursor (psaD) from Spinacia
                  oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133,
                  gb_N65521, gb_T42498, gb_T41918, gb_N38024
Seq. No.
                  163872
                  LIB3177-069-P1-K1-A4
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g4454036
BLAST score 535
E value 9.0e-55
Match length 106
% identity 94

NCBI Description (AL035394) putative major latex protein [Arabidopsis

thalianal

Seq. No. 163873

Seq. ID LIB3177-069-P1-K1-A5

Method BLASTN NCBI GI g3869062



BLAST score 148
E value 8.0e-78
Match length 231
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K11I1, complete sequence [Arabidopsis thaliana]

Seq. No. 163874

Seq. ID LIB3177-069-P1-K1-A7

Method BLASTX
NCBI GI g2462929
BLAST score 413
E value 9.0e-41
Match length 87

% identity 93

NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No. 163875

Seq. ID LIB3177-069-P1-K1-A9

Method BLASTX
NCBI GI g3157924
BLAST score 315
E value 5.0e-29
Match length 80
% identity 78

NCBI Description (AC002131) Contains homology to extensin-like protein

gb_D83227 from Populus nigra. ESTs gb_H76425, gb_T13883, gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb_Z25951

come from this gene. There is a similar ORF on the

opposite strand. [... >gi_4063707 (AF104327) extensin-like

protein [Arabidopsis thaliana]

Seq. No. 163876

Seq. ID LIB3177-069-P1-K1-B11

Method BLASTX
NCBI GI g1168607
BLAST score 601
E value 1.0e-62
Match length 118
% identity 98

NCBI Description AUXIN-INDUCED PROTEIN AUX2-11 >gi_16197_emb_CAA37526

(X53435) Aux2-11 protein [Arabidopsis thaliana] >gi_454285 (L15450) auxin-responsive protein [Arabidopsis thaliana]

Seq. No. 163877

Seq. ID LIB3177-069-P1-K1-B12

Method BLASTN
NCBI GI g3927822
BLAST score 324
E value 0.0e+00
Match length 446
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F8N16 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 163878

Seq. ID LIB3177-069-P1-K1-B2



Method BLASTX
NCBI GI g3242075
BLAST score 299
E value 1.0e-27
Match length 56
% identity 100

NCBI Description (Z97059) S-adenosyl-L-homocysteine hydrolase [Arabidopsis

thaliana]

Seq. No. 163879

Seq. ID LIB3177-069-P1-K1-B3

Method BLASTX
NCBI GI g132074
BLAST score 718
E value 3.0e-76
Match length 134
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1

ribulose-bisphosphate carboxylase (\overline{EC} 4. $\overline{1.1.39}$) small chain

Al precursor - Arabidopsis thaliana

Seq. No. 163880

Seq. ID LIB3177-069-P1-K1-B4

Method BLASTN
NCBI GI g2264316
BLAST score 180
E value 1.0e-96
Match length 437
% identity 40

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRO11, complete sequence [Arabidopsis thaliana]

Seq. No. 163881

Seq. ID LIB3177-069-P1-K1-B5

Method BLASTN
NCBI GI g2288979
BLAST score 315
E value 1.0e-177
Match length 348

Match length 348 % identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC T01024 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 163882

Seq. ID LIB3177-069-P1-K1-B6

Method BLASTX
NCBI GI g132074
BLAST score 460
E value 3.0e-46
Match length 103
% identity 88

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR

(RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1

ribulose-bisphosphate carboxylase (\overline{EC} 4. $\overline{1.1.39}$) small chain

Al precursor - Arabidopsis thaliana



```
Seq. No.
                  163883
                  LIB3177-069-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4263525
BLAST score
                   602
                  1.0e-62
E value
Match length
                  141
% identity
                  85
                  (AC004044) putative photosystem I reaction center subunit
NCBI Description
                  II precursor [Arabidopsis thaliana]
Seq. No.
                  163884
Seq. ID
                  LIB3177-069-P1-K1-C11
                  BLASTX
Method
NCBI GI
                  q2052379
BLAST score
                  571
E value
                   4.0e-59
Match length
                  106
% identity
                   99
NCBI Description
                 (U66343) calreticulin [Arabidopsis thaliana]
                  163885
Seq. No.
Seq. ID
                  LIB3177-069-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1653089
BLAST score
                  243
                   1.0e-20
E value
Match length
                  80
% identity
                   56
                  (D90911) hypothetical protein [Synechocystis sp.]
NCBI Description
                  163886
Seq. No.
                  LIB3177-069-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406816
                   545
BLAST score
                  9.0e-59
E value
Match length
                  119
                   97
% identity
                 (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]
NCBI Description
                  163887
Seq. No.
                  LIB3177-069-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132110
BLAST score
                   670
E value
                  1.0e-70
Match length
                  125
                   98
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
```

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 163888

E value

Match length

8.0e-67

128



```
LIB3177-069-P1-K1-C4
Seq. ID
Method
                    BLASTX
NCBI GI
                    g228408
BLAST score
                    633
E value
                    3.0e-66
Match length
                    124
                    66
% identity
NCBI Description calmodulin 1 [Arabidopsis thaliana]
                    163889
Seq. No.
                    LIB3177-069-P1-K1-C6
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1076708
BLAST score
                    657
                    4.0e-69
E value
Match length
                    141
                    27
% identity
                    seed tetraubiquitin - common sunflower
NCBI Description
                    >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max] >gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max] >gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin
                    [Helianthus annuus] >gi_994785_dbj_BAA05085_
                                                                       (D26092)
                    Ubiquitin [Glycine max] \rightarrow gi_4263514_gb_AAD15340_ (AC004044)
                    putative polyubiquitin [Arabidopsis thaliana]
                    >gi_1096513_prf__2111434A tetraubiquitin [Helianthus
                    annuus]
                    163890
Seq. No.
                    LIB3177-069-P1-K1-D1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q1362029
BLAST score
                    374
                    5.0e-36
E value
Match length
                    89
                    72
% identity
NCBI Description
                    thioglucosidase (EC 3.2.3.1) precursor - rape
                    >gi 840725 emb CAA55685 (X79080) myrosinase [Brassica
                    napus]
Seq. No.
                    163891
Seq. ID
                    LIB3177-069-P1-K1-D10
Method
                    BLASTX
NCBI GI
                    q4115364
BLAST score
                    429
E value
                    2.0e-42
Match length
                    97
% identity
NCBI Description
                    (AC005957) putative fatty acid elongase [Arabidopsis
                    thaliana]
Seq. No.
                    163892
Seq. ID
                    LIB3177-069-P1-K1-D11
Method
                    BLASTX
NCBI GI
                    g3953473
BLAST score
                    637
```



% identity 100

NCBI Description (AC002328) F2202.18 [Arabidopsis thaliana]

Seq. No. 163893

Seq. ID LIB3177-069-P1-K1-D12

Method BLASTX
NCBI GI g2764941
BLAST score 518
E value 7.0e-53
Match length 87
% identity 100

NCBI Description (X98255) transcriptionally stimulated by gibberellins;

expressed in meristematic region, and style [Arabidopsis

thaliana]

Seq. No. 163894

Seq. ID LIB3177-069-P1-K1-D2

Method BLASTX
NCBI GI 93894183
BLAST score 458
E value 9.0e-46
Match length 130
% identity 74

NCBI Description (AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No. 163895

Seq. ID LIB3177-069-P1-K1-D3

Method BLASTX
NCBI GI g4138912
BLAST score 140
E value 8.0e-09
Match length 31
% identity 77

NCBI Description (AF059487) expansin precursor [Lycopersicon esculentum]

Seq. No. 163896

Seq. ID LIB3177-069-P1-K1-D4

Method BLASTX
NCBI GI g2118220
BLAST score 235
E value 4.0e-20
Match length 67
% identity 75

NCBI Description H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain

(clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16

kDa proteolipid [Arabidopsis thaliana]

>gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar

H+-transporting ATPase 16K chain [Arabidopsis thaliana]
>gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting
ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]
>gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar
H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No. 163897

Seq. ID LIB3177-069-P1-K1-D8

```
Method
                  BLASTX
NCBI GI
                  g4490325
BLAST score
                  461
                  4.0e-46
E value
                  115
Match length
% identity
                  77
NCBI Description (AL035656) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  163898
                  LIB3177-069-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4544387
BLAST score
                  248
E value
                  1.0e-21
Match length
                  67
                  76
% identity
                 (AC007047) putative purple acid phosphatase precursor
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  163899
Seq. ID
                  LIB3177-069-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1169278
BLAST score
                  361
                  2.0e-34
E value
Match length
                  152
% identity
                  54
NCBI Description DEHYDRIN ERD14 >gi_556474 dbj_BAA04569 (D17715) ERD14
                  protein [Arabidopsis thaliana]
Seq. No.
                  163900
Seq. ID
                  LIB3177-069-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q99735
BLAST score
                  587
                  5.0e-61
E value
Match length
                  112
                  99
% identity
NCBI Description
                 L-ascorbate peroxidase (EC 1.11.1.11) precursor -
                  Arabidopsis thaliana (fragment)
                  163901
Seq. No.
                  LIB3177-069-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4585882
BLAST score
                  578
E value
                  8.0e-60
Match length
                  112
% identity
                  100
                 (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  163902
                  LIB3177-069-P1-K1-E3
```

Seq. ID Method BLASTX

NCBI GI g585165 BLAST score 692



```
E value
                   3.0e-73
Match length
                   145
                   88
% identity
NCBI Description
```

GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM

(G6PD) >gi_2129985_pir__S60287 glucose-6-phosphate

1-dehydrogenase (EC 1.1.1.49) - potato

>gi_471345 emb_CAA52442_ (X74421) glucose-6-phosphate

1-dehydrogenase [Solanum tuberosum]

Seq. No. 163903 Seq. ID

LIB3177-069-P1-K1-E8

Method BLASTX NCBI GI g4587564 BLAST score 575 E value 1.0e-59 Match length 129 90 % identity

NCBI Description (AC006550) Strong similarity to gb X14017 photosystem I

> reaction centre subunit II precursor (psaD) from Spinacia oleracea. ESTs gb R30423, gb T42998, gb Z18178, gb T14133,

gb N65521, gb T42498, gb T41918, gb N38024

163904 Seq. No.

LIB3177-069-P1-K1-E9 Seq. ID

Method BLASTX NCBI GI g2199574 BLAST score 295 E value 4.0e-27 Match length 61 90 % identity

NCBI Description (AF004293) aquaporin [Brassica rapa]

Seq. No.

163905

LIB3177-069-P1-K1-F1 Seq. ID Method BLASTX NCBI GI g1362051

BLAST score 452 E value 5.0e-45Match length 95 92 % identity

NCBI Description protein kinase 3 - soybean >gi 310582 (L19361) protein

kinase 3 [Glycine max]

Seq. No. 163906

LIB3177-069-P1-K1-F10 Seq. ID

Method BLASTN NCBI GI q3046854 BLAST score 346 E value 0.0e + 00Match length 378 98 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRG7, complete sequence [Arabidopsis thaliana]

Seq. No. 163907

LIB3177-069-P1-K1-F11 Seq. ID

Method BLASTX



```
NCBI GI
                   g4585935
BLAST score
                   300
E value
                   1.0e-27
Match length
                   69
% identity
                   86
NCBI Description
                   (AC007211) putative chlorophyll A/B binding protein
                   [Arabidopsis thaliana] >gi 4741946 gb AAD28770.1 AF134123 1
                   (AF134123) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                   163908
Seq. ID
                  LIB3177-069-P1-K1-F12
Method
                  BLASTX
NCBI GI
                   g2341034
BLAST score
                   460
E value
                   4.0e-46
                   92
Match length
% identity
                   100
                  (AC000104) F19P19.13 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  163909
                  LIB3177-069-P1-K1-F2
Seq. ID
Method
                  BLASTN
NCBI GI
                   g240069
BLAST score
                   70
E value
                   7.0e-32
                  70
Match length
% identity
                   100
NCBI Description
                  light-regulated glutamine synthetase isoenzyme [Arabidopsis
                  thaliana, mRNA, 1548 nt]
Seq. No.
                  163910
                  LIB3177-069-P1-K1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3046854
BLAST score
                   161
E value
                   2.0e-85
Match length
                  288
% identity
                   90
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRG7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163911
Seq. ID
                  LIB3177-069-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g1169128
BLAST score
                  196
E value
                  1.0e-15
Match length
                  45
                  82
% identity
                  SERINE/THREONINE-PROTEIN KINASE CTR1 >gi 166680 (L08789)
NCBI Description
                  protein kinase [Arabidopsis thaliana] >gi 166682 (L08790)
                  protein kinase [Arabidopsis thaliana]
```

Seq. No. 163912

Seq. ID LIB3177-069-P1-K1-G1

Method BLASTX NCBI GI g4512675



```
BLAST score
                  794
                  4.0e-85
E value
Match length
                  152
% identity
                  100
                  (AC006931) putative citrate synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  163913
                  LIB3177-069-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g16374
BLAST score
                  305
E value
                  2.0e-28
Match length
                  62
                  89
% identity
NCBI Description
                  (X03908) chlorophyll a/b binding protein (LHCP AB 180)
                  [Arabidopsis thaliana]
Seq. No.
                  163914
                  LIB3177-069-P1-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3236479
BLAST score
                  89
E value
                  1.0e-42
Match length
                  137
% identity
                  91
                  Arabidopsis thaliana BAC F9H3, from chromosome IV near 18.8
NCBI Description
                  cM, complete sequence
Seq. No.
                  163915
                  LIB3177-069-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2956690
BLAST score
                  420
E value
                  3.0e-41
                  127
Match length
                  54
% identity
NCBI Description
                  (AJ223306) PSBY [Arabidopsis thaliana] >gi 3414928
                  (AF079800) PsbY precursor [Arabidopsis thaliana]
                  163916
Seq. No.
                  LIB3177-069-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3157924
BLAST score
                  315
E value
                  6.0e-29
Match length
                  80
% identity
                  78
NCBI Description
                  (AC002131) Contains homology to extensin-like protein
                  gb_D83227 from Populus nigra. ESTs gb_H76425, gb_T13883,
                  gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb_Z25951
                  come from this gene. There is a similar ORF on the
```

opposite strand. [... >gi 4063707 (AF104327) extensin-like

protein [Arabidopsis thaliana]

Seq. No. 163917

Seq. ID LIB3177-069-P1-K1-G5

Method BLASTX

BLAST score

E value

439

1.0e-43



```
NCBI GI
                  g4587542
BLAST score
                  339
                  2.0e-32
E value
Match length
                  73
% identity
                  90
                  (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase
NCBI Description
                  with GDSL-motif family. ESTs gb T45815, gb T45130 and
                  gb Z38046 come from this gene. [Arabidopsis thaliana]
                  163918
Seq. No.
                  LIB3177-069-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3785991
BLAST score
                  329
                  6.0e-31
E value
Match length
                  73
% identity
                  89
NCBI Description (AC005560) putative MAP kinase [Arabidopsis thaliana]
Seq. No.
                  163919
                  LIB3177-069-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1769907
BLAST score
                  454
                  2.0e-45
E value
Match length
                  121
                  76
% identity
NCBI Description
                 (X92975) xyloglucan endo-transglycosylase [Arabidopsis
                  thaliana]
                  163920
Seq. No.
                  LIB3177-069-P1-K1-G8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2961378
                  255
BLAST score
                  1.0e-22
E value
                  60
Match length
% identity
                  42
NCBI Description (AL022141) putative protein [Arabidopsis thaliana]
                  163921
Seq. No.
                  LIB3177-069-P1-K1-G9
Seq. ID
                  BLASTN
Method
                  g2264316
NCBI GI
                  103
BLAST score
                  9.0e-51
E value
                  335
Match length
                  42
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRO11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163922
Seq. ID
                  LIB3177-069-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q115783
```



Match length 95 % identity 89

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 163923

Seq. ID LIB3177-069-P1-K1-H11

Method BLASTX
NCBI GI g3914117
BLAST score 582
E value 3.0e-60
Match length 144
% identity 81

NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE II PRECURSOR (NDK II) (NDP

KINASE II) >gi 3093480 (AF017640) nucleoside diphosphate

kinase type 2 [Arabidopsis thaliana]

Seq. No. 163924

Seq. ID LIB3177-069-P1-K1-H12

Method BLASTX
NCBI GI g4566505
BLAST score 262
E value 4.0e-23
Match length 84

Match length 84 % identity 60

NCBI Description (AF102868) beta-D-glucan exohydrolase isoenzyme ExoI

[Hordeum vulgare]

Seq. No. 163925

Seq. ID LIB3177-069-P1-K1-H2

Method BLASTX
NCBI GI g3080401
BLAST score 587
E value 7.0e-61
Match length 116
% identity 100

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

>gi_4455265_emb_CAB36801.1_ (AL035527) putative protein

[Arabidopsis thaliana]

Seq. No. 163926

Seq. ID LIB3177-069-P1-K1-H3

Method BLASTN
NCBI GI g3402745
BLAST score 166
E value 3.0e-88
Match length 268
% identity 93

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5

(ESSAII project)

Seq. No. 163927

Seq. ID LIB3177-069-P1-K1-H4

Method BLASTN NCBI GI g4519185

Match length

% identity

118 99

NCBI Description (AC005967) putative NADP-dependent



```
140
BLAST score
                  4.0e-73
E value
Match length
                  192
                  93
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K15015, complete sequence
                  163928
Seq. No.
                  LIB3177-069-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244892
BLAST score
                  189
                  8.0e-15
E value
                  55
Match length
% identity
                  64
                 (Z97338) similarity to cycloartenol synthase [Arabidopsis
NCBI Description
                  thaliana]
                  163929
Seq. No.
                  LIB3177-069-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982285
BLAST score
                  350
E value
                  5.0e-33
                  69
Match length
                  80
% identity
NCBI Description (AF051227) GASA5-like protein [Picea mariana]
                  163930
Seq. No.
                  LIB3177-069-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1899188
BLAST score
                  109
E value
                  8.0e-05
Match length
                  85
                  13
% identity
NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum]
                  163931
Seq. No.
                  LIB3177-069-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3123745
BLAST score
                  411
E value
                  1.0e-41
Match length
                  99
                  87
% identity
NCBI Description (AB013447) aluminum-induced [Brassica napus]
Seq. No.
                  163932
                  LIB3177-070-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4115387
BLAST score
                  587
E value
                  5.0e-61
```



glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No. 163933

LIB3177-070-P1-K1-A10 Seq. ID

Method BLASTX NCBI GI q132110 BLAST score 702 2.0e-74E value 131 Match length % identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi 68060 pir RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 163934

LIB3177-070-P1-K1-A11 Seq. ID

Method BLASTN NCBI GI g4757662 BLAST score 232 1.0e-127 E value Match length 465

100 % identity

Genomic sequence for Arabidopsis thaliana BAC F10B6 from NCBI Description

chromosome I, complete sequence

163935 Seq. No.

LIB3177-070-P1-K1-A12 Seq. ID

Method BLASTN g4314354 NCBI GI BLAST score 21 E value 5.5e-02 196

Match length % identity 89

Arabidopsis thaliana chromosome II BAC T9I22 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

163936 Seq. No.

Seq. ID LIB3177-070-P1-K1-A2

Method BLASTX NCBI GI g2129772 BLAST score 292 E value 1.0e-26 Match length 82 % identity

NCBI Description xyloglucan endotransglycosylase-related protein XTR-7 -

Arabidopsis thaliana >gi_1244760 (U43489) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No. 163937 .

LIB3177-070-P1-K1-A3 Seq. ID

Method BLASTX NCBI GI g132110 BLAST score 546



E value 4.0e-56 Match length 106 % identity 96

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi 68060 pir RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 163938

Seq. ID LIB3177-070-P1-K1-A5

Method BLASTN
NCBI GI g2244991
BLAST score 284
E value 1.0e-158
Match length 466
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contiq

fragment No

Seq. No. 163939

Seq. ID LIB3177-070-P1-K1-A6

Method BLASTX
NCBI GI g3157947
BLAST score 814
E value 2.0e-87
Match length 156
% identity 52

NCBI Description (AC002131) Similar to protein gb Z74962 from Brassica

oleracea which is similar to bacterial YRN1 and HEAHIO proteins. ESTs gb_T21954, gb_T04283, gb_Z37609, gb_N37366, gb_R90704, gb_F15500 and gb F14353 come from this gene.

[Arabidopsis tha

Seq. No. 163940

Seq. ID LIB3177-070-P1-K1-A8

Method BLASTX
NCBI GI g115767
BLAST score 743
E value 4.0e-79
Match length 147
% identity 97

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein $ab16\overline{5}$ - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 163941

Seq. ID LIB3177-070-P1-K1-A9

Method BLASTX
NCBI GI g1170939
BLAST score 554
E value 5.0e-57



Match length 115 % identity 92

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)

>gi 1084408 pir S46540 methionine adenosyltransferase (EC

2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon

esculentum]

Seq. No. 163942

Seq. ID LIB3177-070-P1-K1-B1

Method BLASTX
NCBI GI g1773330
BLAST score 618
E value 2.0e-64
Match length 141
% identity 85

NCBI Description (U80071) glycolate oxidase [Mesembryanthemum crystallinum]

Seq. No. 163943

Seq. ID LIB3177-070-P1-K1-B10

Method BLASTX
NCBI GI g3892704
BLAST score 515
E value 2.0e-52
Match length 93
% identity 100

NCBI Description (AL033545) RCc3-like protein [Arabidopsis thaliana]

Seq. No. 163944

Seq. ID LIB3177-070-P1-K1-B11

Method BLASTX
NCBI GI g115767
BLAST score 790
E value 1.0e-84
Match length 150
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372 emb CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 163945

Seq. ID LIB3177-070-P1-K1-B12

Method BLASTX
NCBI GI g115767
BLAST score 717
E value 4.0e-76
Match length 138
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding



protein (LHCP AB 65) [Arabidopsis thaliana]
>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 163946

Seq. ID LIB3177-070-P1-K1-B2

Method BLASTN
NCBI GI g14342
BLAST score 316
E value 1.0e-178
Match length 316
% identity 100

NCBI Description A.thaliana mRNA for carbonic anhydrase

Seq. No. 163947

Seq. ID LIB3177-070-P1-K1-B3

Method BLASTX
NCBI GI g115767
BLAST score 649
E value 4.0e-68
Match length 126
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi 16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541 (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 163948

Seq. ID LIB3177-070-P1-K1-B4

Method BLASTX
NCBI GI g3915865
BLAST score 414
E value 1.0e-40
Match length 102
% identity 82

NCBI Description 40S RIBOSOMAL PROTEIN S4

Seq. No. 163949

Seq. ID LIB3177-070-P1-K1-B5

Method BLASTX
NCBI GI g132110
BLAST score 731
E value 1.0e-77
Match length 138
% identity 97

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR

(RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_(X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 163950

Seq. ID LIB3177-070-P1-K1-B6



```
Method
                  BLASTX
NCBI GI
                  g2443751
BLAST score
                  802
                  5.0e-86
E value
                  159
Match length
                  100
% identity
NCBI Description
                  (AF020303) fumarase [Arabidopsis thaliana] >qi 2529676
                  (AC002535) putative fumarase [Arabidopsis thaliana]
                  163951
Seq. No.
                  LIB3177-070-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g99696
BLAST score
                  691
                  4.0e-73
E value
Match length
                  134
                  99
% identity
NCBI Description
                  glutamate--ammonia ligase (EC 6.3.1.2) precursor,
                  chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana
                  >gi 240070 bbs 69728 (S69727) light-regulated glutamine
                  synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430
                  aa] [Arabidopsis thaliana] >gi 228453 prf 1804333A Gln
                  synthetase [Arabidopsis thaliana]
                  163952
Seq. No.
                  LIB3177-070-P1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4263642
BLAST score
                  423
E value
                  0.0e + 00
                  431
Match length
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC T13H18 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  163953
Seq. No.
Seq. ID
                  LIB3177-070-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  q2194121
BLAST score
                  612
E value
                  1.0e-65
Match length
                  134
% identity
                  92
                  (AC002062) Strong similarity to Arabidopsis cyclin delta-1
NCBI Description
                   (gb_ATCD1). EST gb_ATTS4338 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  163954
Seq. ID
                  LIB3177-070-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  q541858
BLAST score
                  785
```

Method BLASTX
NCBI GI g541858
BLAST score 785
E value 4.0e-84
Match length 148
% identity 99

NCBI Description endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan



transferase [Arabidopsis thaliana] $>gi_4063757$ (ACO05561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No. 163955

Seq. ID LIB3177-070-P1-K1-C10

Method BLASTX
NCBI GI g1169201
BLAST score 414
E value 1.0e-40
Match length 109
% identity 80

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR

>gi_421830_pir__S33707 DRT112 protein - Arabidopsis

thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No. 163956

Seq. ID LIB3177-070-P1-K1-C11

Method BLASTX
NCBI GI g399307
BLAST score 451
E value 6.0e-45
Match length 143
% identity 61

NCBI Description PRENYL TRANSFERASE >gi 99282 pir A40433 prephytoene

pyrophosphatase dehydrogenase (crtE) homolog - Cyanophora paradoxa >gi_336639 (M37111) prephytoene pyrophosphate dehydrogenase [Cyanophora paradoxa] >gi_1016130 (U30821)

prenyl transferase [Cyanophora paradoxa]

Seq. No. 163957

Seq. ID LIB3177-070-P1-K1-C2

Method BLASTX
NCBI GI g1350680
BLAST score 770
E value 3.0e-82
Match length 149
% identity 99

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 163958

Seq. ID LIB3177-070-P1-K1-C3

Method BLASTX
NCBI GI g3608142
BLAST score 252
E value 1.0e-21
Match length 126
% identity 43

NCBI Description (AC005314) putative hin1 [Arabidopsis thaliana]

Seq. No. 163959

Seq. ID LIB3177-070-P1-K1-C5

Method BLASTX
NCBI GI g131398
BLAST score 546
E value 5.0e-56
Match length 140
% identity 80



NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR

>gi_72714_pir__F2MU10 photosystem II 10K protein precursor

- Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)

photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
>gi_3152571 (AC002986) Match to photosystem II 10kDa
polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,
gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

Seq. No. 163960

Seq. ID LIB3177-070-P1-K1-C6

Method BLASTX
NCBI GI g2384696
BLAST score 394
E value 3.0e-38
Match length 159
% identity 51

NCBI Description (AF013216) acyl-CoA oxidase [Myxococcus xanthus]

come from this gene. [Arabidopsis

Seq. No. 163961

Seq. ID LIB3177-070-P1-K1-C7

Method BLASTX
NCBI GI g2119846
BLAST score 605
E value 4.0e-63
Match length 117

% identity 97

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 163962

Seq. ID LIB3177-070-P1-K1-C8

Method BLASTX
NCBI GI g1732570
BLAST score 156
E value 2.0e-10
Match length 33
% identity 94

NCBI Description (U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No. 163963

Seq. ID LIB3177-070-P1-K1-C9

Method BLASTX
NCBI GI g115385
BLAST score 447
E value 1.0e-44
Match length 105
% identity 87

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

```
Seq. No.
                   163964
Seq. ID
                   LIB3177-070-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   q3286693
BLAST score
                   790
E value
                   1.0e-84
Match length
                   156
                   100
% identity
NCBI Description (Y15433) 33 kDa polypeptide of oxygen-evolving complex
                   (OEC) in photosystem II [Arabidopsis thaliana]
Seq. No.
                   163965
Seq. ID
                  LIB3177-070-P1-K1-D11
Method
                   BLASTN
NCBI GI
                   g2244870
BLAST score
                   270
E value
                   1.0e-150
Match length
                   288
                   92
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
                  163966
Seq. No.
Seq. ID
                  LIB3177-070-P1-K1-D12
Method
                  BLASTX
NCBI GI
                   g3024434
BLAST score
                   528
E value
                   6.0e-54
Match length
                  126
                   86
% identity
NCBI Description
                  26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
                   PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_
                   (D88663) Tat binding protein 1 [Brassica rapa]
Seq. No.
                   163967
Seq. ID
                  LIB3177-070-P1-K1-D3
Method
                  BLASTX
NCBI GI
                   a2388710
BLAST score
                   393
E value
                   3.0e - 38
Match length
                  110
% identity
                   68
                  (AF017150) betaine aldehyde dehydrogenase [Amaranthus
NCBI Description
                  hypochondriacus]
Seq. No.
                  163968
Seq. ID
                  LIB3177-070-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g1922944
BLAST score
                  306
E value
                  5.0e-28
Match length
                  84
                  76
% identity
NCBI Description
                  (AC000106) Strong similarity to Picea histone H2A
```

21915

this gene. [Arabidopsis thaliana]

(gb_X67819). ESTs gb_ATTS3874,gb_T46627,gb_T14194 come from



Seq. No. 163969

Seq. ID LIB3177-070-P1-K1-D8

Method BLASTX
NCBI GI g132102
BLAST score 686
E value 2.0e-72
Match length 131
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR

(RUBISCO SMALL SUBUNIT 2B) >gi 68061 pir RKMUB2

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_(X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

Seq. No. 163970

Seq. ID LIB3177-070-P1-K1-D9

Method BLASTX
NCBI GI g1709687
BLAST score 543
E value 6.0e-56
Match length 109
% identity 96

NCBI Description PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O)

REDUCTASE) >gi_2129643_pir__S71275 methionine sulfoxide reductase - Arabidopsis thaliana >gi_1279212_emb_CAA65991_

(X97326) methionine sulfoxide reductase [Arabidopsis

thaliana]

Seq. No. 163971

Seq. ID LIB3177-070-P1-K1-E1

Method BLASTX
NCBI GI 94741954
BLAST score 706
E value 8.0e-75
Match length 148
% identity 91

NCBI Description (AF134127) Lhcb4.2 protein [Arabidopsis thaliana]

Seq. No. 163972

Seq. ID LIB3177-070-P1-K1-E10

Method BLASTX
NCBI GI g4680651
BLAST score 215
E value 3.0e-17
Match length 138
% identity 38

NCBI Description (AF132940) CGI-06 protein [Homo sapiens]

Seq. No. 163973

Seq. ID LIB3177-070-P1-K1-E11

Method BLASTN
NCBI GI g4584351
BLAST score 456
E value 0.0e+00
Match length 456

% identity

NCBI Description

65

[Arabidopsis thaliana]



% identity 100 NCBI Description Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence Seq. No. 163974 Seq. ID LIB3177-070-P1-K1-E12 Method BLASTN NCBI GI g4199934 BLAST score 35 E value 5.0e-10 Match length 597 % identity 53 Genomic sequence for Arabidopsis thaliana BAC T3P18, NCBI Description complete sequence [Arabidopsis thaliana] Seq. No. 163975 Seq. ID LIB3177-070-P1-K1-E2 Method BLASTX NCBI GI q4741948 BLAST score 776 E value 5.0e-83 Match length 146 % identity 100 NCBI Description (AF134124) Lhcb2 protein [Arabidopsis thaliana] Seq. No. 163976 LIB3177-070-P1-K1-E3 Seq. ID Method BLASTX NCBI GI q3204108 BLAST score 656 E value 6.0e-69 Match length 136 % identity 89 NCBI Description (AJ006764) putative deoxycytidylate deaminase [Cicer arietinum] Seq. No. 163977 Seq. ID LIB3177-070-P1-K1-E4 Method BLASTX g1769905 NCBI GI BLAST score 569 E value 1.0e-58 Match length 149 % identity 74 (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) NCBI Description [Arabidopsis thaliana] Seq. No. 163978 Seq. ID LIB3177-070-P1-K1-E5 Method BLASTX NCBI GI q1769905 BLAST score 205 E value 1.0e-16 Match length 65

21917

(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)



```
Seq. No.
                  163979
                  LIB3177-070-P1-K1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2656031
BLAST score
                  80
E value
                   4.0e-37
Match length
                  156
% identity
                  88
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC20
Seq. No.
                  163980
Seq. ID
                  LIB3177-070-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q4835233
BLAST score
                  425
E value
                  6.0e-42
Match length
                  95
                  93
% identity
NCBI Description
                  (AL049862) putative protein 1 photosystem II
                  oxygen-evolving complex [Arabidopsis thaliana]
                  163981
Seq. No.
                  LIB3177-070-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129538
BLAST score
                  53
E value
                  5.0e-16
Match length
                  50
                  88
% identity
NCBI Description AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232)
                  AT103 [Arabidopsis thaliana]
Seq. No.
                  163982
Seq. ID
                  LIB3177-070-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g2129538
BLAST score
                  265
E value
                  3.0e-23
Match length
                  51
% identity
                  100
NCBI Description AT103 protein - Arabidopsis thaliana >gi 1033195 (U38232)
                  AT103 [Arabidopsis thaliana]
Seq. No.
                  163983
                  LIB3177-070-P1-K1-F10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4584531
BLAST score
                  469
E value
                  0.0e+00
Match length
                  481
% identity
                  30
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8
```

Seq. No. 163984

(ESSA project)



```
Seq. ID
                   LIB3177-070-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   q4741940
BLAST score
                   385
                   2.0e-37
E value
Match length
                   71
% identity
                   99
NCBI Description
                 (AF134120) Lhca2 protein [Arabidopsis thaliana]
Seq. No.
                   163985
                  LIB3177-070-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244979
BLAST score
                   647
E value
                   7.0e-68
Match length
                   132
                   99
% identity
NCBI Description
                  (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis
                  thaliana]
Seq. No.
                   163986
                  LIB3177-070-P1-K1-F2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3449332
BLAST score
                   401
E value
                  0.0e+00
Match length
                   449
% identity
                  99
                 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSF19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  163987
                  LIB3177-070-P1-K1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1532162
BLAST score
                  145
E value
                  5.0e-76
Match length
                  169
% identity
                  96
NCBI Description Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3,
                  AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14
                  genes, partial cds, AT.I.24-7, ascorbate peroxidase
                   (ATHAPX1), EF-lalpha-A1, -A2 and -A3 (EF-lalpha) and AT.I
Seq. No.
                  163988
Seq. ID
                  LIB3177-070-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g464987
BLAST score
                  629
E value
                  1.0e-65
Match length
                  116
% identity
                  100
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN
```

21919

>gi_421858_pir__S32672 ubiquitin--protein ligase (EC
6.3.2.19) UBC10 - Arabidopsis thaliana
>gi_297878_emb_CAA78715 (Z14991) ubiquitin conjugating

LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)

% identity

NCBI Description

62



enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin
conjugating enzyme [Arabidopsis thaliana]

```
Seq. No.
                   163989
Seq. ID
                   LIB3177-070-P1-K1-F6
Method
                   BLASTN
NCBI GI
                   g1209241
BLAST score
                   124
E value
                   1.0e-63
Match length
                   184
% identity
                   92
NCBI Description Arabidopsis thaliana metallothionein mRNA sequence
Seq. No.
                   163990
Seq. ID
                  LIB3177-070-P1-K1-F8
Method
                  BLASTX
NCBI GI
                   q2764941
BLAST score
                   607
E value
                   3.0e-63
Match length
                   106
% identity
                   100
                   (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                   expressed in meristematic region, and style [Arabidopsis
                  thaliana]
Seq. No.
                   163991
Seq. ID
                  LIB3177-070-P1-K1-F9
Method
                  BLASTX
NCBI GI
                   g2129752
BLAST score
                   413
E value
                   2.0e-40
Match length
                   86
% identity
                   97
                  thioredoxin - Arabidopsis thaliana >gi 992964_emb_CAA84612_
NCBI Description
                   (Z35475) thioredoxin [Arabidopsis thaliana]
Seq. No.
                  163992
Seq. ID
                  LIB3177-070-P1-K1-G1
Method
                  BLASTN
NCBI GI
                  g3449323
BLAST score
                   364
E value
                   0.0e+00
Match length
                   368
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MZA15, complete sequence [Arabidopsis thaliana]
Seq. No.
                   163993
Seq. ID
                  LIB3177-070-P1-K1-G11
Method
                  BLASTN
NCBI GI
                  g4519195
BLAST score
                  98
E value
                  1.0e-47
Match length
                  146
```

21920

MQC12, complete sequence

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

```
Seq. No.
                   163994
Seq. ID
                   LIB3177-070-P1-K1-G2
Method
                  BLASTN
NCBI GI
                   g4756963
BLAST score
                   231
E value
                   1.0e-127
Match length
                   459
% identity
                   99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
                   (ESSA project)
Seq. No.
                   163995
Seq. ID
                  LIB3177-070-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q1351271
BLAST score
                  185
E value
                   9.0e-14
Match length
                   41
% identity
                   90
                  TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                   >gi_1084309_pir__S52032 triose-phosphate isomerase (EC
                   5.3.1.1) precursor, chloroplast - spinach >gi 806312
                   (L36387) triosephosphate isomerase, chloroplast isozyme
                   [Spinacia oleracea]
Seq. No.
                  163996
Seq. ID
                  LIB3177-070-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g4741960
BLAST score
                  500
E value
                  1.0e-50
Match length
                  116
% identity
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                  163997
Seq. ID
                  LIB3177-070-P1-K1-G5
Method
                  BLASTN
NCBI GI
                  g4567237
BLAST score
                  404
E value
                  0.0e+00
Match length
                  478
% identity
                  100
NCBI Description Arabidopsis thaliana chromosome II BAC T22F11 genomic
                  sequence, complete sequence
Seq. No.
                  163998
Seq. ID
                  LIB3177-070-P1-K1-G6
Method
                  BLASTN
NCBI GI
                  g2749918
BLAST score
                  215
E value
                  1.0e-117
Match length
                  295
% identity
                  98
```

sequence, complete sequence [Arabidopsis thaliana]

NCBI Description Arabidopsis thaliana chromosome I BAC F316 genomic



Seq. No. 163999

Seq. ID LIB3177-070-P1-K1-G7

Method BLASTX
NCBI GI g2062164
BLAST score 520
E value 4.0e-53
Match length 100
% identity 100

NCBI Description (AC001645) jasmonate inducible protein isolog [Arabidopsis

thaliana]

Seq. No. 164000

Seq. ID LIB3177-070-P1-K1-G8

Method BLASTN
NCBI GI g3452262
BLAST score 473
E value 0.0e+00
Match length 473
% identity 100

NCBI Description Arabidopsis thaliana phosphatidylinositol 4-kinase mRNA,

partial cds

Seq. No. 164001

Seq. ID LIB3177-070-P1-K1-G9

Method BLASTX
NCBI GI g1361982
BLAST score 623
E value 4.0e-65
Match length 150
% identity 84

NCBI Description 4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis

thaliana >gi_609340 (U18675) 4-coumarate--coenzyme A ligase

[Arabidopsis thaliana]

Seq. No. 164002

Seq. ID LIB3177-070-P1-K1-H1

Method BLASTX
NCBI GI g115767
BLAST score 208
E value 1.0e-16
Match length 92
% identity 54

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll

a/b-binding protein $ab16\overline{5}$ - Arabidopsis thaliana

>gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No. 164003

Seq. ID LIB3177-070-P1-K1-H10

Method BLASTX NCBI GI g4454036 BLAST score 624 E value 3.0e-65



```
Match length
                  129
% identity
NCBI Description
                  (AL035394) putative major latex protein [Arabidopsis
                  thaliana]
                  164004
Seq. No.
                  LIB3177-070-P1-K1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3047074
BLAST score
                  44
E value
                  1.0e-15
Match length
                  120
% identity
                  84
NCBI Description Arabidopsis thaliana BAC F21E10
Seq. No.
                  164005
Seq. ID
                  LIB3177-070-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g3860247
BLAST score
                  450
E value
                  6.0e-45
Match length
                  92
                  93
% identity
NCBI Description
                 (AC005824) unknown protein [Arabidopsis thaliana]
                  164006
Seq. No.
Seq. ID
                  LIB3177-070-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q4468807
BLAST score
                  569
E value
                  6.0e-64
Match length
                  142
% identity
                  84
NCBI Description
                 (AL035601) cytochrome P450 monooxygenase-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  164007
Seq. ID
                  LIB3177-070-P1-K1-H4
Method
                  BLASTN
NCBI GI
                  q4220637
BLAST score
                  419
E value
                  0.0e+00
Match length
                  423
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MIE1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  164008
Seq. ID
                  LIB3177-070-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  q3047074
BLAST score
                  439
```

Method BLASTN
NCBI GI g3047074
BLAST score 439
E value 0.0e+00
Match length 439
% identity 100

NCBI Description Arabidopsis thaliana BAC F21E10